

## BLAST Basic Local Alignment Search Tool

Job Title: Nucleotide sequence (1713 letters)

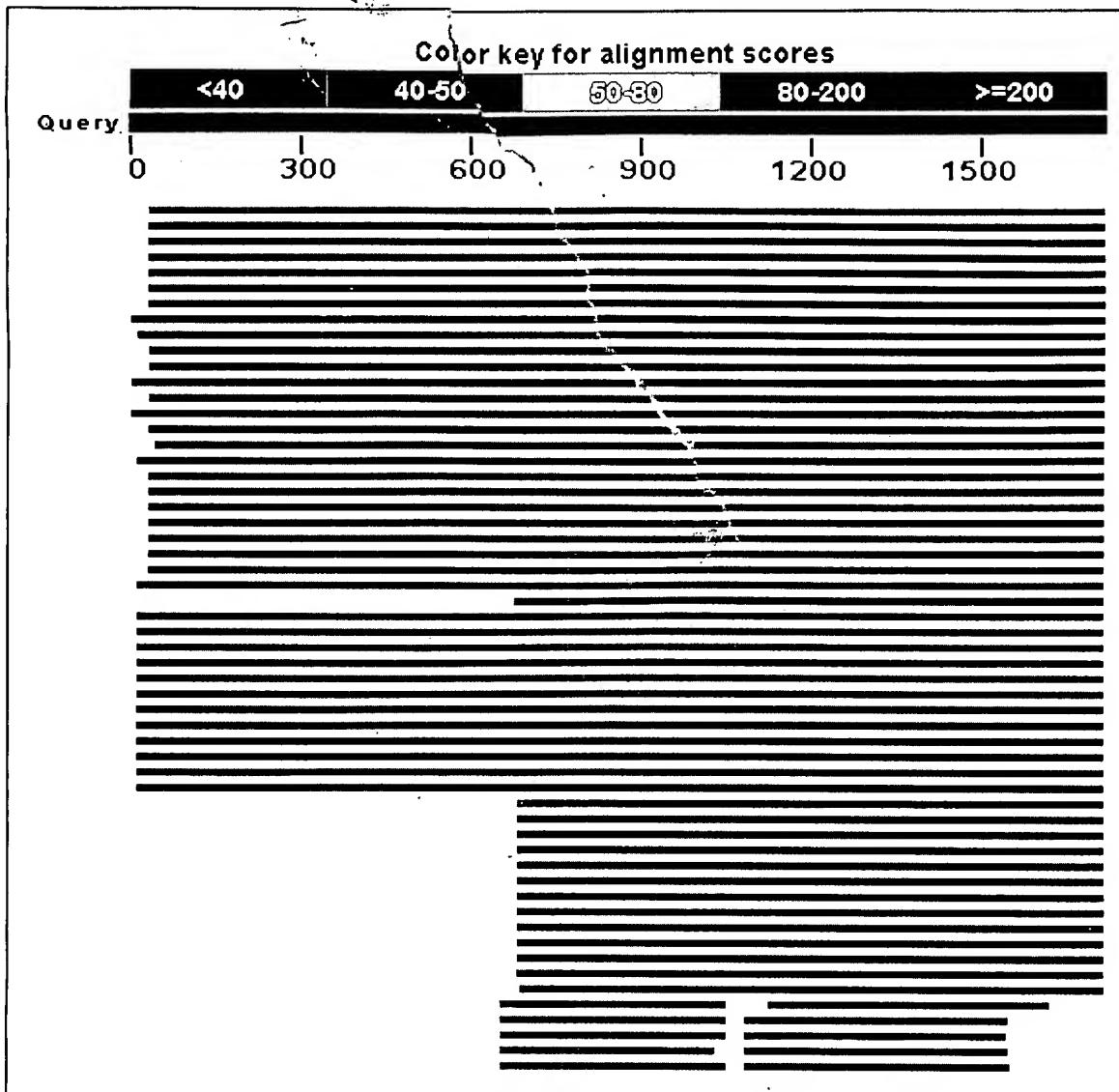
32

•  
•  
•  
BLASTN 2.2.17 (Aug-26-2007)

RID: HT584ZYV012 Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences) 6,012,929 sequences; 22,005,976,730 total letters

Query= Length=1713

SEQ ID NO: 6

Distribution of 100 Blast Hits on the Query Sequence

## Distance tree of results NEW

 Legend for links to other resources: **U** UniGene **E** GEO **G** Gene **S** Structure **M** Map Viewer

## Sequences producing significant alignments:

(Click headers to sort columns)

AY973860.1	Hepatitis C virus isolate cs2a-4 polyprotein gene, NS5B RNA dependent RNA polymerase region, partial cds	3092	3092	97%	0.0	99%
AY973859.1	Hepatitis C virus isolate cs2a-1 polyprotein gene, NS5B RNA dependent RNA polymerase region, partial cds	3075	3075	97%	0.0	99%
AF177036.1	Hepatitis C virus subtype 2a strain HC-J6CH clone pJ6CF, complete genome	3075	3075	97%	0.0	99%
AY973858.1	Hepatitis C virus isolate 2a-con polyprotein gene, NS5B RNA dependent RNA polymerase region, partial cds	3014	3014	97%	0.0	99%
D00944.1	Hepatitis C virus genomic RNA for polyprotein, complete cds	2737	2737	97%	0.0	96%
AB047641.1	Hepatitis C virus gene for polyprotein, complete cds, clone:JCH-2	2643	2643	97%	0.0	95%
AB047645.1	Hepatitis C virus gene for polyprotein, complete cds, clone:JCH-6	2549	2549	97%	0.0	94%
AF238483.1	Hepatitis C virus subtype 2a strain MD2a-4, complete genome	2523	2523	99%	0.0	93%
AY746460.1	Hepatitis C virus genotype 2a polyprotein gene, complete cds	2499	2499	98%	0.0	93%
AF238484.1	Hepatitis C virus subtype 2a strain MD2a-5, complete genome	2494	2494	97%	0.0	93%
AF169003.1	Hepatitis C virus subtype 2a isolate G2aK1, complete genome	2490	2490	97%	0.0	93%
AB047640.1	Hepatitis C virus gene for polyprotein, complete cds, clone:JCH-1	2488	2488	99%	0.0	92%
AF238482.1	Hepatitis C virus subtype 2a strain MD2a-2, complete genome	2477	2477	97%	0.0	93%
AF169005.1	Hepatitis C virus subtype 2a isolate NDM59, complete genome	2475	2475	99%	0.0	92%
AF238481.1	Hepatitis C virus subtype 2a strain MD2a-1, complete genome	2471	2471	97%	0.0	93%
AF169002.1	Hepatitis C virus subtype 2a isolate NDM228, complete genome	2470	2470	97%	0.0	93%
AF238485.1	Hepatitis C virus subtype 2a strain MD2a-7, complete genome	2455	2455	98%	0.0	92%
AB047644.1	Hepatitis C virus gene for polyprotein, complete cds, clone:JCH-5	2444	2444	97%	0.0	92%
AF169004.1	Hepatitis C virus subtype 2a isolate G2aK3, complete genome	2440	2440	97%	0.0	92%
AB047642.1	Hepatitis C virus gene for polyprotein, complete cds, clone:JCH-3	2438	2438	97%	0.0	92%
AB047643.1	Hepatitis C virus gene for polyprotein, complete cds, clone:JCH-4	2383	2383	97%	0.0	92%
AB237837.1	Hepatitis C virus full-length replicon pFGR-JFH1 RNA, complete sequence	2344	2344	97%	0.0	91%
AB047639.1	Hepatitis C virus (isolate JFH-1) genomic RNA, complete genome	2344	2344	97%	0.0	91%
AB114136.1		2344	2344	97%	0.0	91%

Hepatitis C virus replicon pSGR-JFH1 gene for neomycin resistance gene product, hepatitis C virus nonstructural protein, complete cds

AB031663.1	Hepatitis C virus (isolate VAT96) genomic RNA, complete genome	1596	1596	98%	0.0	83%
D10076.1	Hepatitis C virus (HCV) genomic RNA, 3'-terminal part of NS5 region	1570	1570	60%	0.0	94%
D50409.1	Hepatitis C virus (isolate BEBE1) genomic RNA, complete genome	1563	1563	98%	0.0	83%
DQ155561.1	Hepatitis C virus (isolate D54) polyprotein gene, partial cds	1539	1539	98%	0.0	83%
AY232731.1	Hepatitis C virus clone MD2b1-2 polyprotein mRNA, complete cds	1491	1491	98%	0.0	82%
AY232730.1	Hepatitis C virus clone MD2b1-1 polyprotein mRNA, complete cds	1480	1480	98%	0.0	82%
AY232743.1	Hepatitis C virus clone MD2b7-2 polyprotein mRNA, complete cds	1447	1447	98%	0.0	82%
AY232742.1	Hepatitis C virus clone MD2b7-1 polyprotein mRNA, complete cds	1447	1447	98%	0.0	82%
AY232738.1	Hepatitis C virus clone MD2b5-1 polyprotein mRNA, complete cds	1413	1413	98%	0.0	81%
AY232735.1	Hepatitis C virus clone MD2b3-2 polyprotein mRNA, complete cds	1408	1408	98%	0.0	81%
D10988.1	Hepatitis C virus genome	1402	1402	98%	0.0	81%
AY232739.1	Hepatitis C virus clone MD2b5-2 polyprotein mRNA, complete cds	1397	1397	98%	0.0	81%
AY232737.1	Hepatitis C virus clone MD2b4-2 polyprotein mRNA, complete cds	1397	1397	98%	0.0	81%
AY232734.1	Hepatitis C virus clone MD2b3-1 polyprotein mRNA, complete cds	1363	1363	98%	0.0	81%
D49776.1	Hepatitis C virus isolate JK128 gene for NS5, partial cds	1075	1075	60%	0.0	85%
D86529.1	Hepatitis C virus gene for polyprotein (NS5 region), partial cds and 3'UTR, isolate: BA045	1059	1059	60%	0.0	85%
D49777.1	Hepatitis C virus isolate JK139 gene for NS5, partial cds	1048	1048	60%	0.0	85%
D84398.1	Hepatitis C virus gene for polyprotein (NS5 region), partial cds, isolate:UD254	1042	1042	60%	0.0	85%
D86532.1	Hepatitis C virus gene for polyprotein (NS5 region), partial cds and 3'UTR, isolate: RU169	1037	1037	60%	0.0	85%
D49769.1	Hepatitis C virus isolate JK081 gene for NS5, partial cds	1037	1037	60%	0.0	85%
D49775.1	Hepatitis C virus isolate JK117 gene for NS5, partial cds	1026	1026	60%	0.0	84%
D49780.1	Hepatitis C virus isolate JK151 gene for NS5, partial cds	1014	1014	60%	0.0	84%
D49761.1	Hepatitis C virus isolate JK025 gene for NS5, partial cds	1014	1014	60%	0.0	84%
D49772.1	Hepatitis C virus isolate JK109 gene for NS5, partial cds	1009	1009	60%	0.0	84%
D49760.1	Hepatitis C virus isolate JK020 gene for NS5, partial cds	1009	1009	60%	0.0	84%
D49778.1	Hepatitis C virus isolate JK143 gene for NS5, partial cds	1003	1003	60%	0.0	84%
D86530.1	Hepatitis C virus gene for polyprotein (NS5 region), partial cds and 3'UTR, isolate: BA047	948	948	59%	0.0	83%

AB284202.1	Hepatitis C virus subtype 6a gene for polyprotein (NS5B region), partial cds, isolate: TV137	741	741	28%	0.0	93%
AB281370.1	Hepatitis C virus gene for polyprotein (NS5B region), partial cds, isolate: VT368	702	702	26%	0.0	94%
AB281423.1	Hepatitis C virus gene for polyprotein (NS5B region), partial cds, isolate: VT538	686	686	26%	0.0	93%
AB281394.1	Hepatitis C virus gene for polyprotein (NS5B region), partial cds, isolate: VT449	686	686	26%	0.0	93%
AB281369.1	Hepatitis C virus gene for polyprotein (NS5B region), partial cds, isolate: VT130	680	680	27%	0.0	93%
AB281376.1	Hepatitis C virus gene for polyprotein (NS5B region), partial cds, isolate: VT399	675	675	27%	0.0	92%
AB284218.1	Hepatitis C virus subtype 2a gene for polyprotein (NS5B region), partial cds, isolate: TV158	671	671	26%	0.0	92%
AB284192.1	Hepatitis C virus subtype 2a gene for polyprotein (NS5B region), partial cds, isolate: TV124	669	669	26%	0.0	93%
AB281402.1	Hepatitis C virus gene for polyprotein (NS5B region), partial cds, isolate: VT475	664	664	27%	0.0	92%
AB284203.1	Hepatitis C virus subtype 2a gene for polyprotein (NS5B region), partial cds, isolate: TV138	662	662	25%	0.0	93%
AB281410.1	Hepatitis C virus gene for polyprotein (NS5B region), partial cds, isolate: VT503	658	658	26%	0.0	92%
DQ238634.1	Hepatitis C virus isolate DON11 NS5B protein (NS5B) gene, partial cds	652	652	23%	0.0	95%
U14293.1	Hepatitis C virus 2a K33 RNA polymerase (ns5) gene, partial cds	649	649	24%	0.0	94%
AB281407.1	Hepatitis C virus gene for polyprotein (NS5B region), partial cds, isolate: VT496	643	643	27%	0.0	91%
U14294.1	Hepatitis C virus 2a K43 RNA polymerase (ns5) gene, partial cds	643	643	24%	0.0	94%
AB281381.1	Hepatitis C virus gene for polyprotein (NS5B region), partial cds, isolate: VT420	636	636	27%	1e-178	91%
DQ238705.1	Hepatitis C virus isolate DON97 NS5B protein (NS5B) gene, partial cds	636	636	23%	1e-178	94%
AB284228.1	Hepatitis C virus subtype 2a gene for polyprotein (NS5B region), partial cds, isolate: TV106	614	614	24%	5e-172	92%
AB284249.1	Hepatitis C virus subtype 2a gene for polyprotein (NS5B region), partial cds, isolate: VT550	588	588	23%	3e-164	93%
AY004015.1	Hepatitis C virus isolate IDU189 clone II non-structural protein 5b gene, partial cds	580	580	23%	5e-162	92%
AY004016.1	Hepatitis C virus isolate IDU189 clone III non-structural protein 5b gene, partial cds	575	575	23%	2e-160	92%
AY004014.1	Hepatitis C virus isolate IDU189 clone I non-structural protein 5b gene, partial cds	575	575	23%	2e-160	92%
AY834959.1	Hepatitis C virus isolate gb32 NS5b protein gene, partial cds	573	573	21%	8e-160	93%
U14288.1	Hepatitis C virus 2a I27 RNA polymerase (ns5) gene, partial cds	571	571	24%	3e-159	91%
AY004017.1	Hepatitis C virus isolate IDU189 clone IV non-structural protein 5b gene, partial cds	569	569	23%	1e-158	92%
AY834970.1	Hepatitis C virus isolate bj1 NS5b protein gene, partial cds	569	569	21%	1e-158	93%
AY834955.1	Hepatitis C virus isolate bj165 NS5b protein gene, partial cds	568	568	21%	4e-158	93%
DQ220940.1	Hepatitis C virus isolate G2MP031 NS5B (NS5B) gene, partial cds	566	566	22%	1e-157	92%

D28848.1	Hepatitis C virus RNA for NS5, partial sequence	566	566	21%	1e-157	94%
AY834956.1	Hepatitis C virus isolate bj779 NS5b protein gene, partial cds	564	564	21%	5e-157	93%
AY834957.1	Hepatitis C virus isolate bj665 NS5b protein gene, partial cds	562	562	21%	2e-156	93%
AY834969.1	Hepatitis C virus isolate sz450 NS5b protein gene, partial cds	558	558	21%	2e-155	93%
DQ220938.1	Hepatitis C virus isolate G2MP043 NS5B (NS5B) gene, partial cds	549	549	22%	1e-152	91%
AB284240.1	Hepatitis C virus subtype 2a gene for polyprotein (NS5B region), partial cds, isolate: VT96	547	547	27%	5e-152	87%
AY834958.1	Hepatitis C virus isolate bj688 NS5b protein gene, partial cds	547	547	21%	5e-152	92%
AY834967.1	Hepatitis C virus isolate gz2 NS5b protein gene, partial cds	545	545	21%	2e-151	92%
AB284236.1	Hepatitis C virus subtype 2a gene for polyprotein (NS5B region), partial cds, isolate: VT909	544	544	21%	6e-151	93%
AY834968.1	Hepatitis C virus isolate km49 NS5b protein gene, partial cds	540	540	21%	8e-150	92%
DQ220931.1	Hepatitis C virus isolate G2MP034 NS5B (NS5B) gene, partial cds	536	536	22%	1e-148	91%
AY834965.1	Hepatitis C virus isolate zz12 NS5b protein gene, partial cds	536	536	21%	1e-148	91%
AY834961.1	Hepatitis C virus isolate sy7 NS5b protein gene, partial cds	536	536	21%	1e-148	92%
DQ220939.1	Hepatitis C virus isolate G2MP040 NS5B (NS5B) gene, partial cds	531	531	22%	5e-147	91%
DQ220926.1	Hepatitis C virus isolate G2MP029 NS5B (NS5B) gene, partial cds	531	531	22%	5e-147	91%
AY834964.1	Hepatitis C virus isolate bj675 NS5b protein gene, partial cds	531	531	21%	5e-147	92%
AY834960.1	Hepatitis C virus isolate zz4 NS5b protein gene, partial cds	531	531	21%	5e-147	92%
DQ220937.1	Hepatitis C virus isolate G2MP038 NS5B (NS5B) gene, partial cds	529	529	22%	2e-146	89%
D14190.1	Hepatitis C virus gene for NS5, partial cds, isolate SR103	529	529	19%	2e-146	94%
AY834963.1	Hepatitis C virus isolate km46 NS5b protein gene, partial cds	527	527	21%	6e-146	91%
AY834971.1	Hepatitis C virus isolate gz6 NS5b protein gene, partial cds	525	525	21%	2e-145	91%

## Alignments

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>gb|AY973860.1| Hepatitis C virus isolate cs2a-4 polyprotein gene, NS5B RNA dependent RNA polymerase region, partial cds  
Length=1770

Score = 3092 bits (1674), Expect = 0.0  
Identities = 1676/1677 (99%), Gaps = 0/1677 (0%)  
Strand=Plus/Plus

Query 37	ACTCCTTGTAGTCCCGAAGAGGAGAAGTTACCGATTAACCCCTTGAGCAACTCCCTGTTG	96
Sbjct 28	.....	87
Query 97	CGATATCACACAAGGTGTACTGTACCACAACAAAGAGCGCCTCACTAAGGGCTAAAAG	156
Sbjct 88	.....	147
Query 157	GTAACTTTGATAGGATGCAÄGTGCTCGACTCCTACTACGACTCAGTCTAAAGGACATT	216
Sbjct 148	.....	207
Query 217	AAGCTAGCGGCCTCCAAGGTACCCGAAGGCTCCTCACCATGGAGGAGGCTTGCCAGTTA	276
Sbjct 208	.....	267
Query 277	ACCCCACCCATTCTGCAAGATCTAAATATGGGTTGGGCTAAGGAGGTCCGAGCTTG	336
Sbjct 268	.....	327
Query 337	TCCGGGAGGGCCGTTAACACACATCAAGTCCGTGTGAAAGGACCTCCTGGAGGACTCAGAA	396
Sbjct 328	.....	387
Query 397	ACACCAATTCCCACAACCATTATGCCAAAAATGAGGTGTTCTGCGTGGACCCCACCAAG	456
Sbjct 388	.....	447
Query 457	GGGGGCAAGAAAGCAGCTCGCCTTATCGTTACCCCTGACCTCGCGTCAGGGTCTGCGAG	516
Sbjct 448	.....	507
Query 517	AAGATGGCCCTTATGACATTACACAAAAACTCCTCAGGCGGTGATGGGGCTTCTTAT	576
Sbjct 508	.....	567
Query 577	GGATTCCAGTATTCCCCCGCTCAGCGGGTAGAGTTCTCTTGAAAGCATGGCGGAAAG	636
Sbjct 568	.....	627
Query 637	AAGGACCCTATGGGTTTTCGTATGATAACCGATGCTTGACTCAACCGTCACTGAGAGA	696
Sbjct 628	.....	687
Query 697	GACATCAGGACTGAGGAGTCATATATCGGGCCTGCTCCTGCCAGGAGGCCACACT	756
Sbjct 688	.....	747
Query 757	GCCATACACTCGCTAACTGAGAGACTTACGTGGGAGGCCTATGTTAACAGCAAGGGC	816
Sbjct 748	.....	807
Query 817	CAAACCTGCGGGTACAGGCATTGCCCGCCAGCGGGGTGCTCACCACTAGCATGGGAAC	876
Sbjct 808	.....	867
Query 877	ACCATCACATGCTACGTGAAAGCCTTAGCGGCTTGTAAAGCTGCAGGGATAATCGCGCCC	936
Sbjct 868	.....	927
Query 937	ACAATGCTGGTATGCCCGATGACTTGGTTGTCATCTCAGAAAGCCAGGGGACCGAGGAG	996
Sbjct 928	.....	987
Query 997	GACGAGCGAACCTGAGAGCCTCACGGAGGCTATGACCAGGTATTCTGCCCTCCTGGT	1056
Sbjct 988	.....	1047
Query 1057	GAcccccccAGACCGGAGTATGATCTGGAGCTGATAACATCTGCTCCTCAAATGTGTCT	1116
Sbjct 1048	.....	1107
Query 1117	GTGGCGCTGGGCCACAAGGCCGCCAGATACTACCTGACCAGAGACCTACCACTCCA	1176
Sbjct 1108	.....	1167
Query 1177	ATCGCCCGGGCTGCCTGGAAACAGTTAGACACTCCCCTGTCAATTGAGCTGGAAAC	1236
Sbjct 1168	.....	1227
Query 1237	ATCATCCAGTACGCCCGACCATATGGCTCGCATGGCCTGATGACACACTTCTTCTCC	1296
Sbjct 1228	.....	1287
Query 1297	ATTCTCATGGCTCAAGACACGCTGGACCAGAACCTCAACTTGAGATGTACGGAGCGGTG	1356

Sbjct	1288	.....	1347
Query	1357	TACTCCGTGAGTCCCTGGACCTCCCAGCTATAATTGAAAGGTTACATGGGCTTGACGCT	1416
Sbjct	1348	.....	1407
Query	1417	TTTTCTCTGCACACATACTCCCCACGAAC TGACACGGGTGGCTTCAGCCCTCAGAAAA	1476
Sbjct	1408	.....	1467
Query	1477	CTTGGGGCGCCACCCCTCAGAGCGTGGAAAGAGCCGGCACGTGCAGTCAGGGCGTCCCTC	1536
Sbjct	1468	.....	1527
Query	1537	ATCTCCC GTGGGGGAGAGCGGCCGTCTCGGGTCGATATCTCTTCAACTGGCGGTGAAG	1596
Sbjct	1528	.....	1587
Query	1597	ACCAAGCTCAA ACTCACTCCATTGCCGGAGGCGCGCCTCCTGGATTATCCAGCTGGTTC	1656
Sbjct	1588	.....	1647
Query	1657	ACCGTCGGCGCCGGCGGGGCGACATTATCACAGCGTGTGCGTGCCGACACGC	1713
Sbjct	1648	.....C...	1704

>gb|AY973859.1| Hepatitis C virus isolate cs2a-1 polyprotein gene, NS5B RNA dependent RNA polymerase region, partial cds  
Length=1761

Score = 3075 bits (1665), Expect = 0.0  
Identities = 1673/1677 (99%), Gaps = 0/1677 (0%)  
Strand=Plus/Plus

Query	37	ACTCCTTGTAGTCCCGAAGAGGAGAACGATTAACCCCTTGAGCAACTCCCTGTTG	96
Sbjct	19	.....	78
Query	97	CGATATCACAACAAGGTGTACTGTACCAACAAAGAGCGCCTCACTAAGGGCTAAAAG	156
Sbjct	79	.....C.....	138
Query	157	GTAACTTTGATAGGATGCAAGTGCTCGACTCCTACTACGACTCAGTCTAAAGGACATT	216
Sbjct	139	.....	198
Query	217	AAGCTAGCGGCCTCCAAGGTACCGCAAGGCTCCTCACCATGGAGGAGGCTGCCAGTTA	276
Sbjct	199	.....	258
Query	277	ACCCCACCCATTCTGCAAGATCTAAATATGGTTGGGCTAAGGAGGTCCGCAGCTTG	336
Sbjct	259	.....	318
Query	337	TCCGGGAGGGCCGTTAACCATCAAGTCCGTGGAAGGACCTCCTGGAGGACTCAGAA	396
Sbjct	319	.....	378
Query	397	ACACCAATTCCCACAACCATTATGCCAAAAATGAGGTGTTCTGCGTGGACCCCACCAAG	456
Sbjct	379	.....	438
Query	457	GGGGGCAAGAAAGCAGCTGCCTTATCGTTACCCGTACCTCGCGTCAGGGCTGCGAG	516
Sbjct	439	.....G.....	498
Query	517	AAGATGGCCCTTTATGACATTACACAAAAACTTCCTCAGGCGGTGATGGGGCTTCTTAT	576
Sbjct	499	.....	558
Query	577	GGATTCCAGTATTCCCCGCTCAGCGGGTAGAGTTCTTGTAAAGCATGGCGGAAAAG	636
Sbjct	559	.....	618
Query	637	AAGGACCTATGGTTTCTGATGACATTACACAAAAACTTCCTCAGGCGGTGATGGGGCTTCTTAT	696
Sbjct	619	.....	678
Query	697	GACATCAGGACTGAGGAGTCCATATATCGGGCCTGCTCCTGCCAGGAGGCCACACT	756
Sbjct	679	.....	738
Query	757	GCCATACACTCGCTAACTGAGAGACTTACGTGGAGGGCTATGTTAACAGCAAGGGC	816
Sbjct	739	.....	798
Query	817	CAAACCTGCGGGTACAGGC GTTGCCCGCCAGCGGGGTGCTCACCCTAGCATGGGAAC	876
Sbjct	799	.....	858
Query	877	ACCATCACATGCTACGTGAAAGCCTTAGCGGTTGTAAAGCTGCAGGGATAATCGGCC	936
Sbjct	859	.....	918
Query	937	ACAATGCTGGTATGCGCGATGACTTGGTTGTCACTCAGAAAGCCAGGGACCGAGGAG	996
Sbjct	919	.....	978
Query	997	GACGAGCGAACCTGAGAGCCTCACGGAGGCTATGACCAAGGTATTCTGCCCTCCTGGT	1056
Sbjct	979	.....	1038
Query	1057	GACcccccccAGACCGGAGTATGATCTGGAGCTGATAACATCTGCTCCTCAAATGTGTCT	1116

Sbjct	1039	.....	1098
Query	1117	GTGGCGCTGGGCCACAAGGCCGCCAGATACTACCTGACCAGAGACCTACCACTCCA	1176
Sbjct	1099	.....	1158
Query	1177	ATCGCCCGGGCTGCCTGGAAACAGTTAGACACTCCCCTGTCAATTATGGCTGGAAAC	1236
Sbjct	1159	.....	1218
Query	1237	ATCATCCAGTACGCCCGACCATATGGGCTCGCATGGCCTGATGACACACTTCTCTCC	1296
Sbjct	1219	.....	1278
Query	1297	ATTCTCATGGCTCAAGACACGCTGGACCAGAACCTCAACTTGAGATGTACGGAGCGGTG	1356
Sbjct	1279	.....	1338
Query	1357	TACTCCGTGAGTCCCTGGACCTCCCAGCTATAATTGAAAGGTTACATGGCCTGACGCT	1416
Sbjct	1339	.....	1398
Query	1417	TTTTCTCTGCACACATACACTCCCCACGAACGTGACACGGGTGGCTTCAGCCCTCAGAAAA	1476
Sbjct	1399	.....	1458
Query	1477	CTTGGGGGCCACCCCTCAGAGCGTGGAAAGAGCCGGGCACGTGCAGTCAGGGCGTCCCTC	1536
Sbjct	1459	.....	1518
Query	1537	ATCTCCC GTGGGGGAGAGCGGCCGTCTCGGGTCGATATCTCTTCAACTGGCGGTGAAG	1596
Sbjct	1519	.....T.....	1578
Query	1597	ACCAAGCTCAAACACTCCATTGCCGGAGGC GCGCCTCCTGGATTATCCAGCTGGTTC	1656
Sbjct	1579	.....	1638
Query	1657	ACCGTCGGCGCCGGCGGGGCGACATTATCACAGCGTGT CGGTGCCCGACCACGC	1713
Sbjct	1639	.....C.....	1695

>gb|AF177036.1| Hepatitis C virus subtype 2a strain HC-J6CH clone pJ6CF, complete genome  
Length=9711

Score = 3075 bits (1665), Expect = 0.0  
Identities = 1673/1677 (99%), Gaps = 0/1677 (0%)  
Strand=Plus/Plus

Query	37	ACTCCTTGTAGTCCCGAAGAGGGAGTTACCGATTAACCCCTTGAGCAACTCCCTGTTG	96
Sbjct	7700	.....	7759
Query	97	CGATATCACACAAAGGTGTACTGTACCAACAAAGAGCGCCTCACTAAGGGCTAAAAG	156
Sbjct	7760	.....	7819
Query	157	GTAACCTTTGATAGGATGCAAGTGCCTCGACTCCTACTACGACTCAGTCTAAAGGACATT	216
Sbjct	7820	.....	7879
Query	217	AAGCTAGCGGCCTCCAAGGTACCGCAAGGCTCCTCACCATGGAGGAGGCTGCCAGTTA	276
Sbjct	7880	.....	7939
Query	277	ACCCCACCCATTCTGCAAGATCTAAATATGGTTGGGCTAAGGAGGTCCGCAGCTTG	336
Sbjct	7940	.....	7999
Query	337	TCCGGGAGGGCCGTTAACACATCAAGTCCGTGGAAAGGACCTCCTGGAGGACTCAGAA	396
Sbjct	8000	.....	8059
Query	397	ACACCAATTCCCACAACCATTATGCCAAAAATGAGGTGTTCTCGCTGGACCCCACCAAG	456
Sbjct	8060	.....	8119
Query	457	GGGGGCAAGAAAGCAGCTCGCCTTACGTTACCCCTGACCTCGCGTCAGGGCTCGAG	516
Sbjct	8120	.....	8179
Query	517	AAGATGGCCCTTATGACATTACACAAAAACTCCTCAGGC GGATGGGGCTTCTTAT	576
Sbjct	8180	.....	8239
Query	577	GGATTCCAGTATTCCCCCGCTCAGCGGGTAGAGTTCTCTTGAAAGCATGGCGGAAAG	636
Sbjct	8240	.....	8299
Query	637	AAGGACCTATGGGTTTTCGTATGATAACCGATGCTTGACTCAACCGTCACTGAGAGA	696
Sbjct	8300	.....	8359
Query	697	GACATCAGGACTGAGGAGTCCATATATCGGGCCTGCTCCTGCCCGAGGAGGCCACACT	756
Sbjct	8360	.....	8419
Query	757	GCCATACACTCGCTAACTGAGAGACTTACGTGGAGGGCTATGTTCAACAGCAAGGGC	816
Sbjct	8420	.....	8479
Query	817	CAAACCTGCGGGTACAGGC GTTGCCCGCCAGCGGGGTGCTCACCACTAGCATGGGAAC	876

Sbjct	8480	.....	8539
Query	877	ACCATCACATGCTACGTGAAAGCCTAGCGGTTGTAAAGCTGCAGGGATAATCGCGCCC	936
Sbjct	8540	.....	8599
Query	937	ACAATGCTGGTATGC CGCGATGACTTGGTTGTCATCTCAGAAAGCCAGGGGACCGAGGAG	996
Sbjct	8600	.....	8659
Query	997	GACGAGCGGAACCTGAGAGCCTCACGGAGGCTATGACCAGGTATTCTGCCCTCCTGGT	1056
Sbjct	8660	.....	8719
Query	1057	GAcccccccAGACCGGAGTATGATCTGGAGCTGATAACATCTGCTCCTCAAATGTGTCT	1116
Sbjct	8720	.....	8779
Query	1117	GTGGCGCTGGGCCACAAGGCCGCCAGATACTACCTGACCAGAGACCTACCACTCCA	1176
Sbjct	8780	.....	8839
Query	1177	ATCGCCC GGCTGCCTGGAAACAGTTAGACACTCCCCTGTCAATT CATGGCTGGAAAC	1236
Sbjct	8840	.....	8899
Query	1237	ATCATCCAGTACGCCCGACCATATGGGCTCGCATGGCCTGATGACACACTTCTCTCC	1296
Sbjct	8900	.....	8959
Query	1297	ATTCTCATGGCTCAAGACACGCTGGACCAGAACCTCAACTTGAGATGTACGGAGCGGTG	1356
Sbjct	8960	.....	9019
Query	1357	TACTCCGTGAGTCCCTGGACCTCCCAGCTATAATTGAAAGGTTACATGGGCTTGACGCT	1416
Sbjct	9020	.....	9079
Query	1417	TTTCTCTGCACACATAACTCCCCACGAAC TGACACGGGTGGCTTCAGCCCTCAGAAAA	1476
Sbjct	9080	.....	9139
Query	1477	CTTGGGGCGCCACCCCTCAGAGCGTGGAAAGAGCCGGCACGTGCAGTCAGGGCGTCCCTC	1536
Sbjct	9140	.....	9199
Query	1537	ATCTCCGTGGGGGAGAGCGGCCGTCTCGCGTCGATATCTCTTCAACTGGCGGTGAAG	1596
Sbjct	9200	.....T.....T.....	9259
Query	1597	ACCAAGCTCAA ACTCACTCCATTGCCGGAGGC GCGCCTCCTGGATTATCCAGCTGGTTC	1656
Sbjct	9260	.....A.....	9319
Query	1657	ACCGTCGGCGCCGGCGGGGCGACATTATCACAGCGTGT CGGTGCCCGACACGC	1713
Sbjct	9320	.....C...	9376

>gb|AY973858.1| Hepatitis C virus isolate 2a-con polyprotein gene, NS5B RNA dependent RNA polymerase region, partial cds  
Length=1776

Score = 3014 bits (1632), Expect = 0.0  
Identities = 1662/1677 (99%), Gaps = 0/1677 (0%)  
Strand=Plus/Plus

Query	37	ACTCCTTGTAGTCCGAAGAGGAGAAGTTACCGATTAACCCCTTGAGCAACTCCCTGTTG	96
Sbjct	34	.....G.....	93
Query	97	CGATATCACAACAAGGTGTACTGTACCAACAAAGAGCGCCTCACTAAGGGCTAAAAG	156
Sbjct	94	.....C.....	153
Query	157	GTAACCTTTGATAGGATGCAAGTGTGACTCCTACTACGACTCAGTCTAAAGGACATT	216
Sbjct	154	.....T.....	213
Query	217	AAGCTAGCGGCCTCCAAGGTACCGCAAGGCTCCTCACCATGGAGGAGGCTGCCAGTTA	276
Sbjct	214	.....	273
Query	277	ACCCCACCCATTCTGCAAGATCTAAATATGGGTTGGGCTAAGGAGGTCCGCAGCTTG	336
Sbjct	274	.....C.....	333
Query	337	TCCGGGAGGGCCGTTAACCAACATCAAGTCCGTGGAAGGACCTCCTGGAGGACTCAGAA	396
Sbjct	334	.....C..	393
Query	397	ACACCAATTCCCACAACCATTATGCCAAAAATGAGGTGTTCTCGCGTGGACCCCACCAAG	456
Sbjct	394	.....	453
Query	457	GGGGGCAAGAAAGCAGCTCGCCTTATCGTTACCCCTGACCTCGGCGTCAGGGTCTGCGAG	516
Sbjct	454	.....	513
Query	517	AAGATGCCCTTATGACATTACACAAAAACTCCTCAGCGGTGATGGGGCTTCTTAT	576
Sbjct	514	.....	573
Query	577	GGATTCCAGTATTCCCCCGCTCAGCGGGTAGAGTTCTTGAAAGCATGGCGGAAAAG	636

Sbjct	574	.....	633
Query	637	AAGGACCCTATGGGTTTCGTATGATAACCGATGCTTGACTCAACCGTCACTGAGAGA	696
Sbjct	634	.....	693
Query	697	GACATCAGGACTGAGGAGTCCATATATCGGGCCTGCTCCTGCCGAGGAGGCCACACT	756
Sbjct	694	.....	753
Query	757	GCCATACACTCGCTAACGTGAGAGACTTACGTGGGAGGGCTATGTTAACAGCAAGGGC	816
Sbjct	754	.....G.....C...C.....	813
Query	817	CAAACCTGCGGGTACAGGCCTGCGCGCAGCGGGGTGCTCACCCTAGCATGGGAAC	876
Sbjct	814	.....	873
Query	877	ACCATCACATGCTACGTGAAAGCCTAGCGGTTGTAAAGCTGCAGGGATAATCGCGCC	936
Sbjct	874	.....G.....G.....	933
Query	937	ACAATGCTGGTATGCGCGATGACTTGGTTGTCATCTCAGAAAGCCAGGGACCGAGGAG	996
Sbjct	934	..G.....	993
Query	997	GACGAGCGGAACCTGAGAGCCTTCACGGAGGCTATGACCAGGTATTCTGCCCTCCTGGT	1056
Sbjct	994	.....	1053
Query	1057	GAccccccAGACCGGAGTATGATCTGGAGCTGATAACATCTGCTCCTCAAATGTGTCT	1116
Sbjct	1054	.....	1113
Query	1117	GTGGCGCTGGGCCACAAGGCCGCCAGATACTACCTGACCAGAGACCTACCACTCCA	1176
Sbjct	1114	.....	1173
Query	1177	ATCGCCCGGGCTGCCTGGAAACAGTTAGACACTCCCCGTCAATTGATGGCTGGAAAC	1236
Sbjct	1174	.....	1233
Query	1237	ATCATCCAGTACGCCCCGACCATATGGCTCGCATGGCCTGATGACACACTTCTCTCC	1296
Sbjct	1234	.....	1293
Query	1297	ATTCTCATGGCTCAAGACACGCTGGACCAGAACCTCAACTTGAGATGTACGGAGCGGTG	1356
Sbjct	1294	.....T.....T.....	1353
Query	1357	TACTCCGTGAGTCCCTGGACCTCCAGCTATAATTGAAAGGTTACATGGCTTGACGCT	1416
Sbjct	1354	.....	1413
Query	1417	TTTCTCTGCACACATACTCCCCACGAACACTGACACGGTGGCTCAGCCCTCAGAAAA	1476
Sbjct	1414	.....	1473
Query	1477	CTTGGGGGCCACCCCTCAGAGCGTGGAAAGAGCCGGCACGTGCAGTCAGGGTCCCTC	1536
Sbjct	1474	.....	1533
Query	1537	ATCTCCGTGGGGGAGAGCGGCCGTGCGTCGATATCTCTTCAACTGGCGGTGAAG	1596
Sbjct	1534	.....T.....	1593
Query	1597	ACCAAGCTAAACTCACTCATTGCCGGAGGCACGCCTCCTGGATTATCCAGCTGGTTC	1656
Sbjct	1594	.....	1653
Query	1657	ACCGTCGGCGCCGGCGGGGCGACATTACAGCGTGTGCGTGCCTGCCGACACACGC	1713
Sbjct	1654	.....C...C.....	1710

>dbj|D00944.1|HPCPOLP Hepatitis C virus genomic RNA for polyprotein, complete cds  
Length=9589

Score = 2737 bits (1482), Expect = 0.0  
Identities = 1613/1678 (96%), Gaps = 2/1678 (0%)  
Strand=Plus/Plus

Query	37	ACTCCTTGTAGTCCCGAACAGAGGAGAACGTTACCGATTAACCCCTTGAGCAACTCCCTGTTG	96
Sbjct	7700	.....C.....A.....G..A.....	7759
Query	97	CGATATCACAACAAGGTGTACTGTACCAACAAAGAGCGCCTCACTAAGGGCTAAAAAG	156
Sbjct	7760	.....T.....T.....	7819
Query	157	GTAACTTTGATAGGATGCAAGTGCTCGACTC-CTACTACGACTCAGTCTAAAGGACAT	215
Sbjct	7820	.....C.....G.T.-T..T.....G.....	7878
Query	216	TAAGCTAGCGGCCTCCAAGGTACCGCAAGGCTCCTCACCATGGAGGGAGGCTGCCAGTT	275
Sbjct	7879	.....T.....TT.A.....C.....	7938
Query	276	AACCCCACCCATTCTGCAAGATCTAAATATGGGTTGGGCTAAGGAGGTCCGCAGCTT	335
Sbjct	7939	...T.....C.....C..G.....	7998
Query	336	GTCCGGGAGGGCCGTTAACACACATCAAGTCCGTGTGGAAGGACCTCCTGGAGGACTCAGA	395
Sbjct	7999	.....A.....A.....A..C.	8058

Query Sbjct	396 8059	AACACCAATTCCCACAACCATTATGCCAAAAATGAGGTGTTCTGCGTGGACCCACAA .....T.....C.....	455 8118
Query Sbjct	456 8119	GGGGGGCAAGAAAGCAGCTCGCTTATCGTTACCTGACCTCGCGTCAGGGCTGCGA .....T.....	515 8178
Query Sbjct	516 8179	GAAGATGGCCCTTATGACATTACACAAAAACTCCTCAGGCAGGTGATGGGGCTTCTTA ...A.....T..C.....G.....	575 8238
Query Sbjct	576 8239	TGGATTCCAGTATTCCCCGCTCAGCGGGTAGAGTTCTCTTGAAGCATGGCGGAAA .....C.....G.....G.....	635 8298
Query Sbjct	636 8299	GAAGGACCTATGGTTTTCGTATGATAACCGATGCTTACTCAACCGTCACTGAGAG ...A.....	695 8358
Query Sbjct	696 8359	AGACATCAGGACTGAGGAGTCCATATATCGGGCTGCTCCTGCCGAGGAGGCCACAC .....T..T.....	755 8418
Query Sbjct	756 8419	TGCCATACACTCGCTAAGTGGAGACTTACGTGGAGGGCTATGTTCAACAGCAAGGG .....A..G.....C.....	815 8478
Query Sbjct	816 8479	CCAAACCTGCGGGTACAGGCAGTGGCGCCAGCGGGTGCTCACCCTAGCATGGGAA ...G.....T.....	875 8538
Query Sbjct	876 8539	CACCATCACATGCTACGTGAAAGCCTAGCGGCTTGTAAAGCTGCAGGGATAATCGGCC .....T.....C.....G.....T.....	935 8598
Query Sbjct	936 8599	CACAATGCTGGTATCGGGCATGACTTGGTTGTATCTCAGAAAGCCAGGGACCGAGGA .....G.....	995 8658
Query Sbjct	996 8659	GGACGAGCGAACCTGAGAGCCTCACGGAGGCTATGACCAGGTATTCTGCCCTCCTGG .....	1055 8718
Query Sbjct	1056 8719	TGACcccccccAGACCGGAGTATGATCTGGAGCTGATAACATCTGCTCCTCAAATGTGTC .....A.....C.....	1115 8778
Query Sbjct	1116 8779	TGTGGCGCTGGGCCACAAGGCCGCCAGATACTACCTGACCAGAGACCTACCACTCC .....T.....	1175 8838
Query Sbjct	1176 8839	AATCGCCCGGGCTGCCTGGAAACAGTTAGACACTCCCTGTCAATTGATGGCTGGAAA .....	1235 8898
Query Sbjct	1236 8899	CATCATCCAGTACGCCCGACCATATGGCTCGATGGCTGTGACACACTTCTTCTC .....A.....	1295 8958
Query Sbjct	1296 8959	CATTCTCATGGCTCAAGACACGCTGGACCAGAACCTCAACTTGAGATGTACGGAGCGGT .....C.....T..T.....	1355 9018
Query Sbjct	1356 9019	GTACTCCGTGAGTCCCTGGACCTCCCAGCTATAATTGAAAGGTTACATGGCTTGACGC .....C.....C.....	1415 9078
Query Sbjct	1416 9079	TTTTCTCTGCACACATACACTCCCCACGAACGTGACACGGGTGGCTTCAGCCCTCAGAAA ...C.....	1475 9138
Query Sbjct	1476 9139	ACTTGGGGGCCACCCCTCAGAGCGTGGAAAGAGCCGGCACGTGCAGTCAGGGCGTCCCT .....	1535 9198
Query Sbjct	1536 9199	CATCTCCGTGGGGGAGAGCGGCCGTGCGGTGATATCTCTTCAACTGGCGGTGAA .....T.....C.....	1595 9258
Query Sbjct	1596 9259	GACCAAGCTAAACTCACTCCATTGCCGGAGGCAGCCTCTGGATTATCCAGCTGGTT .....A.....	1655 9318
Query Sbjct	1656 9319	CACCGTCGGGCCGGCGGGCGACATTATCACAGCGTGTGCGTGGCCGACACGC ...T.....C...	1713 9376

>dbj|AB047641.1| Hepatitis C virus gene for polyprotein, complete cds, clone:JCH-2  
Length=9659

Score = 2643 bits (1431), Expect = 0.0  
Identities = 1596/1678 (95%), Gaps = 2/1678 (0%)  
Strand=Plus/Plus

Query Sbjct	37 7700	ACTCCTTGTAGTCCCGAAGAGGAGAAGTTACCGATTAACCCCTTGAGCAACTCCCTGTTG .....C.....A.....T.....G.....	96 7759
Query Sbjct	97 7760	CGATATCACACAAAGGTGTACTGTACCAACAAAGAGCGCCTCACTAAGGGCTAAAAG .....C.....T.....G.....	156 7819

Query Sbjct	157	GTAACCTTGATAGGATGCAAGTGCTCGACTCCTACTACGACTCAGTCTAAAGGACATT	216
	7820	.....G.....T.....C	7879
Query Sbjct	217	AAGCTAGCGGCCTCCAAGGTACCGCAAGGCTCCTCACCATGGAGGAGGCTGCCAGTTA	276
	7880	.....T.....A.....T.....A	7939
Query Sbjct	277	ACCCCACCCATTCTGCAAGATCTAAATATGGTTGGGCTAAGGAGGTCCAGCTTG	336
	7940	.....C.....C.....G.....C	7999
Query Sbjct	337	TCCGGGAGGGCCGTTAACCATCAAGTCCGTGGAAGGACCTCCTGGAGGACTCAGAA	396
	8000	.....C..C..G..C..	8059
Query Sbjct	397	ACACCAATTCCCACAACCATTATGCCAAAAATGAGGTGTTCTGCGTGGACCCCACCAAG	456
	8060	.....C.....A	8119
Query Sbjct	457	GGGGGCAAGAAAGCAGCTCGCCTATCGTTACCCCTGACCTCGGCGTCAGGGTCTGCGAG	516
	8120	.....T.....	8179
Query Sbjct	517	AAGATGGCCCTTTATGACATTACACAAAAACTTCCTCAGGCGGTGATGGGGCTTCTTAT	576
	8180	.....TG.C.....C.....A	8239
Query Sbjct	577	GGATTCCAGTATTCCCCCGCTCAGCGGGTAGAGTTCTTGTAAAGCATGGCGGAAAG	636
	8240	.....C.....C.....G.....G	8299
Query Sbjct	637	AAGGACCTATGGTTTTCGTATGATAACCGATGCTTGACTCAACCGTCACTGAGAGA	696
	8300	..A.....A.....C.....C	8359
Query Sbjct	697	GACATCAGGACTGAGGAGTCCATATATCGGGCTGCTCCTGCCAGGAGGCCACACT	756
	8360	.....C.....T..C.....	8419
Query Sbjct	757	GCCATACACTCGCTAACTGAGAGACTTACGTGGGAGGGCTATGTTAACAGCAAGGGC	816
	8420	.....T.....	8479
Query Sbjct	817	CAAACCTGCGGGTACAGGCCTGCGCGCCAGCGGGGTGCTCACCACTAGCATGGGAAC	876
	8480	..GT.....T.....	8539
Query Sbjct	877	ACCATCACATGCTACGTGAAAGCCTAGCGGTTGTAAAGCTGCAGGGATAATCGCGCCC	936
	8540	.....G.....CA.....C.....C..C..G.....G.T.....	8599
Query Sbjct	937	ACAATGCTGGTATCGGGCGATGACTTGGTTGTCATCTCAGAAAGCCAGGGACCGAGGAG	996
	8600	.....C.....	8659
Query Sbjct	997	GACGAGCGAACCTGAGAGCCTCACGGAGGTATGACCAGGTATTCTGCCCTCCTGGT	1056
	8660	..T.....C	8719
Query Sbjct	1057	GAcccccccAGACCGGAGTATGATCT-GGAGCTGATAACATCTGCTCCTCAAATGTGTC	1115
	8720	.....A.....T.....T	8778
Query Sbjct	1116	TGTGGCGCTGGGCCACAAGGCCGCCAGATACTACCTGACCAGAGACCTACCACTCC	1175
	8779	.....T.....	8838
Query Sbjct	1176	AATCGCCCGGGCTGCCTGGAAACAGTTAGACACTCCCTGTCAATTGATGGCTGGAAA	1235
	8839	.....C.....	8898
Query Sbjct	1236	CATCATCCAGTACGCCCGACCATATGGCTCGCATGGCCTGATGACACACTTCTTCTC	1295
	8899	.....	8958
Query Sbjct	1296	CATTCTCATGGCTCAAGACACGCTGGACCAGAACCTCAACTTGAGATGTACGGAGCGGT	1355
	8959	...C.....C.....T.....T.....T.....T	9018
Query Sbjct	1356	GTACTCCGTGAGTCCCTGGACCTCCCAGCTATAATTGAAAGGTTACATGGCTTGACGC	1415
	9019	.....A.....T.....C.....C.....C	9078
Query Sbjct	1416	TTTTCTCTGCACACATACACTCCCCACGAACGTGACACGGGTGGCTTCAGCCCTCAGAAA	1475
	9079	...C.....T.....G.....	9138
Query Sbjct	1476	ACTTGGGGCGCCACCCCTCAGAGCGTGGAAAGAGCCGGCACGTGCAGTCAGGGCGTCCCT	1535
	9139	.....T.....T.....G.....A	9198
Query Sbjct	1536	CATCTCCGTGGGGGAGAGCGGCCGTCTGCGGTGATATCTTCAACTGGCGGTGAA	1595
	9199	.....A.....T.....G.....T.....T	9258
Query Sbjct	1596	GACCAAGCTAAACTCACTCCATTGCCGGAGGCACGCCCTGGATTATCCAGCTGGTT	1655
	9259	A.....	9318
Query Sbjct	1656	CACCGTCGGCGCCGGCGGGCGACATTATCACAGCGTGTGCGTGGCCGACCGACGC	1713
	9319	.....C...	9376

>dbj|AB047645.1| Hepatitis C virus gene for polyprotein, complete cds, clone:JCH-6  
Length=9683

Score = 2549 bits (1380), Expect = 0.0  
 Identities = 1579/1678 (94%), Gaps = 2/1678 (0%)  
 Strand=Plus/Plus

Query Sbjct	37	ACTCCTGTAGTCCCGAAGAGGAGAAGTTACCGATTAACCCCTTGAGCAACTCCCTGTTG	96
	7697	.....C.....A.....G..A.....G.....	7756
Query Sbjct	97	CGATATCACAAACAAGGTGTACTGTACCACAACAAAGAGCGCCTCACTAAGGGCTAAAAG	156
	7757	.....C.....T.....T.G.....	7816
Query Sbjct	157	GTAACTTTGATAGGATGCAAGTGCTCGACTCCTACTACGACTCAGTCTAAAGGACATT	216
	7817	.....A.....T..T.....C	7876
Query Sbjct	217	AAGCTAGCGGCCTCCAAGGTACCGCAAGGCTCCTCACCATGGAGGAGGCTGCCAGTTA	276
	7877	.....G.....T.....G.....A..G	7936
Query Sbjct	277	ACCCCACCCATTCTGCAAGATCTAAATATGGTTGGGCTAAGGAGGTCCGCAGCTTG	336
	7937	..T..G.....C.....C..G.....	7996
Query Sbjct	337	TCCGGGAGGGCCGTTAACCATCAAGTCCGTGGAAGGACCTCCTGGAGGACTCAGAA	396
	7997	A..A.....G.....A.....C..	8056
Query Sbjct	397	ACACCAATTCCCACAACCATTATGCCAAAAATGAGGTGTTCTGCGTGGACCCCACCAAG	456
	8057	.....T.....C.....A.....	8116
Query Sbjct	457	GGGGGCAAGAAAGCAGCTCGCCTTATCGTTACCCCTGACCTCGCGTCAGGGCTGCGAG	516
	8117	.....	8176
Query Sbjct	517	AAGATGGCCCTTATGACATTACACAAAAACTTCCTCAGGCGGTGATGGGGCTTCTTAT	576
	8177	.....TG.C.....G.....	8236
Query Sbjct	577	GGATTCCAGTATTCCCCCGCTCAGCGGGTAGAGTTCTCTTGAAAGCATGGCGGAAAG	636
	8237	..T.....C.....T.....G.....	8296
Query Sbjct	637	AA-GGACCCATGGGTTTCGTATGATACCCGATGCTTACTCAACCGTCACTGAGAG	695
	8297	..A..-.....C.....	8355
Query Sbjct	696	AGACATCAGGACTGAGGAGTCCATATATCGGCCGCTGCTCCTGCCGAGGAGGCCACAC	755
	8356	.....AA.....C.A.....C.....G..	8415
Query Sbjct	756	TGCCATACACTCGCTAACTGAGAGACTTACGTGGAGGGCTATGTTAACAGCAAGGG	815
	8416	.....G.....C.....C.....	8475
Query Sbjct	816	CCAAACCTGCGGGTACAGGCCTGCCGCCAGCGGGTGCTCACCACTAGCATGGGAA	875
	8476	...GT.....	8535
Query Sbjct	876	CACCATCACATGCTACGTGAAAGCCTAGCGGCTTGTAAAGCTGCAGGGATAATCGCGCC	935
	8536	.....T..A.....C.....C..G.....G.A.....	8595
Query Sbjct	936	CACAATGCTGGTATGCCGCATGACTTGGTTGTACAGAAAGCCAGGGACCGAGGA	995
	8596	.....C.....T.....	8655
Query Sbjct	996	GGACGAGCGAACCTGAGAGCCTCACGGAGGCTATGACCAGGTATTCTGCCCTCCTGG	1055
	8656	.....A.....	8715
Query Sbjct	1056	TGACcccccccAGACCGGAGTATGATCTGGAGCTGATAACATCTGCTCCTCAAATGTGTC	1115
	8716	.....A.....C.....T.....	8775
Query Sbjct	1116	TGTGGCGCTGGGCCACAAGGCCGCCAGATACTACCTGACCAGAGACCTACCACTCC	1175
	8776	.....A..C.....G..G.....	8835
Query Sbjct	1176	AATCGCCCGGGCTGCCGGAAACAGTTAGACACTCCCTGTCAATTGAGGGAAA	1235
	8836	...T.....A.....	8895
Query Sbjct	1236	CATCATCCAGTACGCCCGACCATATGGGCTCGATGGCCTGATGACACACTTCTTC	1295
	8896	.....T..A.....T.....	8955
Query Sbjct	1296	CATTCTCATGGCTCAAGACACGCTGGACCAGAACCTCAACTTGAGATGTACGGAGCGGT	1355
	8956	.....T.....C.....T.....	9015
Query Sbjct	1356	GTACTCCGTGAGTCCCTGGACCTCCAGCTATAATTGAAAGGTTACATGGCTTGACGC	1415
	9016	.....T.....C.....C.....G...	9075
Query Sbjct	1416	TTTTCTCTGCACACATACACTCCCCACGAACGACTGACACGGGTGGCTTCAGCCCTCAGAAA	1475
	9076	C.....G.....	9135
Query Sbjct	1476	ACTTGGGGCGCCACCCCTCAGAGCGTGGAAAGAGCCGGCACGTGCAGTCAGGGCGTCCCT	1535
	9136	.....A.....T.....G.....A.....	9195
Query	1536	CATCTCCCGTGGGGAGAGCGGCCGTCTGCCGTGATATCTCTCAAACGGCGGTGAA	1595

Sbjct	9196	.....C.....T.....G.....G	9255
Query	1596	GACCAAGCTAAACTCACTCCATTGCCGGAGGCGCGCCTCCTGGATTATCCAGCTGGTT	1655
Sbjct	9256	.....A.....T.....	9315
Query	1656	CACCGTCGGCGCCGGCGGGGCGACATTATCACAGCGTGTGCGTGCCTGGACCACGC	1713
Sbjct	9316	T.....C...	9373

>gb|AF238483.1| Hepatitis C virus subtype 2a strain MD2a-4, complete genome  
Length=9416

Score = 2523 bits (1366), Expect = 0.0  
Identities = 1596/1710 (93%), Gaps = 6/1710 (0%)  
Strand=Plus/Plus

Query	7	ATGTCGTA-TACATGGACAGGCGCCT-TGATCACTCCTGTAGTCCCAGAGAGGAGAAGT	64
Sbjct	7636	.....C.-.C....C.-.G..C.A..A.....C.....A.....	7693
Query	65	TACCGATTAACCCCTTGAGCAACTCCCTGTCGATATCACAAACAAGGTGTACTGTACCA	124
Sbjct	7694	....A.....GT.....A.....T.	7753
Query	125	CAACAAAGAGCGCCTCACTAAGGGCTAAAAGGTAACTTTGATAGGATGCAAGTGCTCG	184
Sbjct	7754	..T.....T.....G.....C.....C.....	7813
Query	185	ACTCCTACTACGACTCAGTCTAAAGGACATTAAGCTAGCGGCCTCCAAGGTACCGCAA	244
Sbjct	7814	..G..C.T.....C.....T.....GT....	7873
Query	245	GGCTCCTCACCATGGAGGAGGCTTGCCAGTTAACCCCACCCATTCTGCAAGATCTAAAT	304
Sbjct	7874	.....T.A.....C.....G.....C....	7933
Query	305	ATGGGTTGGGGCTAAGGAGGTCCGAGCTTGTCCGGAGGGCCGTTAACACATCAAGT	364
Sbjct	7934	....A.....A.....A.....C.....	7993
Query	365	CCGTGTGGAAGGACCTCCTGGAGGACTCAGAAACACCAATTCCCACAACCATTATGGCCA	424
Sbjct	7994	.....A.....C.....T..G.....C.....	8053
Query	425	AAAATGAGGTGTTCTGCGTGGACCCCACCAAGGGGGCAAGAAAGCAGCTGCCTTATCG	484
Sbjct	8054	.....C.....T.....	8113
Query	485	TTTACCCCTGACCTCGGCGTCAGGGCTGCGAGAAGATGCCCTTTATGACATTACACAAA	544
Sbjct	8114	.....A.....A.....A.....T..C.....	8173
Query	545	AACTTCCTCAGGCGGTGATGGGGCTTCTTATGGATTCCAGTATTCCCCCGCTCAGCGGG	604
Sbjct	8174	..G.....C.....C.....T..A..A....	8233
Query	605	TAGAGTTCTCTGAAAGCATGGCGGAAAGAAGGACCTAT-GGGTTTTCGTATGAT	663
Sbjct	8234	..G.....G.....A.....A.....T.....	8292
Query	664	ACCCGATGCTTGACTCAACCGTCACTGAGAGAGACATCAGGACTGAGGAGTCCATATAT	723
Sbjct	8293	.....A.....A.....C.....	8352
Query	724	CGGGCCTGCTCCTGCCGAGGAGGCCACACTGCCATACACTCGCTAACTGAGAGACTT	783
Sbjct	8353	.....C.....A..T.....T.....G.....	8412
Query	784	TACGTGGAGGGCTATGTTCAACAGCAAGGCCAACCTGCGGTACAGGCCATTGCCGC	843
Sbjct	8413	.....G.....C.....A.....T.....	8472
Query	844	GCCAGCGGGGTGCTACCACTAGCATGGGAACACCATCACATGCTACGTGAAAGCCTTA	903
Sbjct	8473	.....A.....T.....C..	8532
Query	904	GCGGCTTGTAAAGCTGCAGGGATAATCGGCCACAAATGCTGGTATGCGCGATGACTTG	963
Sbjct	8533	..A.....G.....G..T.....C.....	8592
Query	964	GTTGTCATCTCAGAAAGCCAGGGACCGAGGAGGACGAGCGAACCTGAGAGCCTTCACG	1023
Sbjct	8593	.....T.....	8652
Query	1024	GAGGCTATGACCAGGTATTCTGCCCTCCTGGTGA.....AGACCGGAGTATGATCTG	1083
Sbjct	8653	.....T.....A.....C...	8712
Query	1084	GAGCTGATAACATCTGCTCCTCAAATGTGCTGTGGCGCTGGGCCACAAGGCCGCCGC	1143
Sbjct	8713	.....T.....C.....AA.....TG.....	8772
Query	1144	AGATACTACCTGACCAGAGACCCCTACCACTCCAATGCCCGGGCTGCCTGGAAACAGTT	1203
Sbjct	8773	.....C.....T.....	8832
Query	1204	AGACACTCCCTGTCAATTGAGACACACTTCTCCATTCTCATGGCTCAAGACACGCTGGAC	1263
Sbjct	8833	.....A..A.....	8892
Query	1264	GCTCGCATGGCCTGATGACACACTTCTCCATTCTCATGGCTCAAGACACGCTGGAC	1323
Sbjct	8893	.....C.....	8952

Query Sbjct	1324 8953	CAGAACCTCAACTTGGAGATGTACGGAGCGGTGTACTCCGTGAGTCCCTGGACCTCCCA .....T.....T.....T.....T.....T.....	1383 9012
Query Sbjct	1384 9013	GCTATAATTGAAAGGTTACATGGGCTTGACGCTTTCTGCACACATACTCCAC ..C.....C.....C.....C.....T.....	1443 9072
Query Sbjct	1444 9073	GAACTGACACGGGTGGCTTCAGCCCTCAGAAAACATTGGGCGCCACCCCTCAGAGCGTGG .....G.....A.....	1503 9132
Query Sbjct	1504 9133	AAGAGCCGGGACGTGCAGTCAGGGCGTCCCTCATCTCCGTGGGGGAGAGCGGCCGTC .....T.....G.....T.....N.....A.....T	1563 9192
Query Sbjct	1564 9193	TGCGGTCGATATCTCTTCAACTGGCGGTGAAGACCAAGCTCAAACACTCCATTGCCG .....G.....	1623 9252
Query Sbjct	1624 9253	GAGGCGCGCCTCTGGATTATCCAGCTGGTCACCGTCGGCGCCGGCGGGCGACATT .....A.....T.....	1683 9312
Query Sbjct	1684 9313	TATCACAGCGTGTGCGTGCACCACGC 1713 .....C... 9342	

>gb|AY746460.1| Hepatitis C virus genotype 2a polyprotein gene, complete cds  
Length=9689

Score = 2499 bits (1353), Expect = 0.0  
Identities = 1584/1698 (93%), Gaps = 6/1698 (0%)  
Strand=Plus/Plus

Query Sbjct	19 7685	TGGACAGGCGCCT-TGATCACTCCTGTAGTCCCGAAGAGGGAGAAGTTACCGATTAACCC .....-G..C....A.....C.....A.....G...G.C....	77 7743
Query Sbjct	78 7744	CTTGAGCAACTCCCTGTGCGATATCACAACAAGGTGTACTGTACCACAACAAAGAGCGC .....GT.....C.....A.....T.....C...	137 7803
Query Sbjct	138 7804	CTCACTAAGGGCTAAAAGGTAACTTTGATAGGATGCAAGTGCTCGACTCCT-ACTACG .....G....C.....-G..C.T....	196 7862
Query Sbjct	197 7863	ACTCAGTCTTAAAGGACATTAAGCTAGCGGCCTCCAAGGTCAACCGAACGGCTCCTCACCA .....C.....T.....G.....C	256 7922
Query Sbjct	257 7923	TGGAGGAGGCTTGCAGTTAACCCACCCATTCTGCAAGATCTAAATATGGGTTGGGG .....A.....C....T.....C.....	316 7982
Query Sbjct	317 7983	CTAAGGAGGTCCGCAGCTGTCCGGAGGGCGTTAACACACATCAAGTCCGTGTGGAAGG .....G.....	376 8042
Query Sbjct	377 8043	ACCTCCTGGAGGACTCAGAAACACCAATTCCACAACCATTATGCCAAAATGAGGTGT .....A.....C.....C.....A....	436 8102
Query Sbjct	437 8103	TCTGCGTGGACCCCACCAAGGGGGCAAGAAAGCAGCTCGCCTTATCGTTACCCGTAC .....T.....C.....	496 8162
Query Sbjct	497 8163	TCGGCGTCAGGGTCTGCGAGAAGATGGCCTTATGACATTACACAAAAACTCCTCAGG .....TG.C.....G.....	556 8222
Query Sbjct	557 8223	CGGTGATGGGGCTTCTATGGATTCCAGTATTCCCCGCTCAGGGGTAGAGTTCTCT .....C.....G.....	616 8282
Query Sbjct	617 8283	TGAAAGCATGGCGGAAAAGA-AGGACCCATGGGTTTCGTATGATAACCGATGCTTT .....G.....T.....G.....	675 8341
Query Sbjct	676 8342	GACTCAACCGTCACTGAGAGAGACATCAGGACTGAGGAGTCCATATCGGGCCTGCTCC .....T.....C.....	735 8401
Query Sbjct	736 8402	TTGCCCGAGGAGGCCACACTGCCATACACTCGCTAACTGAGAGACTTACGTGGGAGGG C.....	795 8461
Query Sbjct	796 8462	CCTATGTTAACAGCAAGGGCAAACCTGCGGTACAGGCCTTGCGCGCCAGCGGGGTG ..C.....GG.....C.....T.....	855 8521
Query Sbjct	856 8522	CTCACCACTAGCATGGGAACACCATCACATGCTACGTGAAAGCCTTAGCGGCTTGTAAA .....C.....A.....C.....G	915 8581
Query Sbjct	916 8582	GCTGCAGGGATAATCGGCCACAAATGCTGGTATGCGCGATGACTTGGTTGTACATCTCA ..C..C...T..G.T..A....G.....C...C.....G	975 8641
Query Sbjct	976 8642	GAAAGCCAGGGACCGAGGAGGACGAGCGAACCTGAGAGCCTCACGGAGGCTATGACC .....GTT.....G..C.....	1035 8701

Query	1036	AGGTATTCTGCCCTCCTGGTGA.....AGACCGGAGTATGATCTGGAGCTGATAACA	1095
Sbjct	8702	.....C..C.....T.....A..C..C.....A.....	8761
Query	1096	TCTTGCTCCTCAAATGTGTCTGTGGCGCTGGGCCACAAGGCCGCGCAGATACTACCTG	1155
Sbjct	8762	.....T.....C.....A..AA..T.....A..T.....	8821
Query	1156	ACCAAGACCCCTACCACTCCAATGCCCGGGCTGCCTGGAAACAGTTAGACACTCCCCT	1215
Sbjct	8822	.....	8881
Query	1216	GTCAATTCATGGCTGGAAACATCATCCAGTACGCCCGACCATAATGGGCTCGATGGTC	1275
Sbjct	8882	.....T.....T..A.....	8941
Query	1276	CTGATGACACACTTCTCCATTCTCATGGCTCAAGACACGCTGGACCAGAACCTCAAC	1335
Sbjct	8942	.....C.....C.....T.....T.....T.....	9001
Query	1336	TTTGAGATGTACGGAGCGGTGTACTCCGTGAGTCCCTGGACCTCCAGCTATAATTGAA	1395
Sbjct	9002	.....C.....C.....	9061
Query	1396	AGGTTACATGGGCTTGACGCTTTCTCTGCACACATACTCCCCACGAACTGACACGG	1455
Sbjct	9062	...C....C.....C.....T.....G....	9121
Query	1456	GTGGCTTCAGCCCTCAGAAAACCTGGGCGCCACCCCTCAGAGCGTGGAAAGAGCCGGGCA	1515
Sbjct	9122	.....AG.....T.....G.....	9181
Query	1516	CGTGCAGTCAGGGCGTCCTCATCTCCGTGGGGGAGAGCGGCCGTCTGCGGTGATAT	1575
Sbjct	9182	.....T.....A.....A.T.....	9241
Query	1576	CTCTTCAACTGGCGGTGAAGACCAAGCTAAACTCACTCCATTGCCGGAGGCGCGCTC	1635
Sbjct	9242	.....A.....	9301
Query	1636	CTGGATTATCCAGCTGGTCACCGTCGGCGCCGGGGCGACATTATCACAGCGTG	1695
Sbjct	9302	.....T.....	9361
Query	1696	TCGCGTGCCCCGACCACGC	1713
Sbjct	9362	C.....C...	9379

>gb|AF238484.1| Hepatitis C virus subtype 2a strain MD2a-5, complete genome  
Length=9416

Score = 2494 bits (1350), Expect = 0.0  
Identities = 1572/1681 (93%), Gaps = 8/1681 (0%)  
Strand=Plus/Plus

Query	37	ACTCCTTGTAGTCCCAGAGAGGAGTTACCGATTAACCCCTTGAGCAACTCCCTGTTG	96
Sbjct	7666	.....C.....A.....A.....A.....A.....	7725
Query	97	CGATATCACAACAAGGTGTACTGTACCAACAAAGAGCGCCTCACTAAGGGCTAAAAAG	156
Sbjct	7726	.....T...T.....T.G.....	7785
Query	157	GTAACTTTGATAGGATGCAAGTGCTCGACTC-CTACTACGACTCAGTCTTAAAGGACAT	215
Sbjct	7786	.....C.....G.T.-T..T.....	7844
Query	216	TAAGCTAGCGCCTCCAAGGTACCGCAAGGCTCCTCACCATGGAGGAGGCTGCCAGTT	275
Sbjct	7845	C.....G.....A...G.....G.....G..T.....	7904
Query	276	AACCCCACCCATTCTGCAAGATCTAAATATGGTTGGGCTAAGGAGGTCCGAGCTT	335
Sbjct	7905	G..T.....C..G.....	7964
Query	336	GTCCGGAGGGCGTTAACACATCAAGTCCGTGGAAGGACCTCTGGAGGACTCAGA	395
Sbjct	7965	.....A.....C.....	8024
Query	396	AACACCAATTCCCACAACCATTATGCCAAAAATGAGGTGTTCTGCGTGGACCCACAA	455
Sbjct	8025	.....T..G.....C.....	8084
Query	456	GGGGGCAAGAAAGCAGCTCGCCTATCGTTACCTGACCTCGCGTCAGGGCTGCGA	515
Sbjct	8085	.....T.....C.....T.....T.....	8144
Query	516	GAAGATGGCCCTTATGACATTACACAAAAACTCCTCAGCGGTGATGGGGCTTCTTA	575
Sbjct	8145	.....TG.C.....G.....	8204
Query	576	TGGATTCCAGTATTCCCCGCTCAGCGGTAGAGTTTC-TCTTGAAAGCATGGCGGAAA	634
Sbjct	8205	...C.....C.....A.....G.-.C.....G.....	8263
Query	635	AGA-AGGACCCATGGGTTTCTGATGACATACCGATGCTTGACTCAACCGTCAGTGAG	693
Sbjct	8264	...G.-.....T.....	8322
Query	694	AGAGACATCAGGACTGAGGAGTCCATATATGGGCCTGCTCCTGCCAGGGAGGCCAC	753
Sbjct	8323	.....A.....C.AA..T..T.....G.	8382
Query	754	ACTGCCATACACTCGCTAAGTGAGAGACTTACGTGGGAGGGCTATGTTAACAGCAAG	813

Sbjct	8383	.....T.....G.....C..C.....T.....	8442
Query Sbjct	814 8443	GGCCAAACCTGCGGGTACAGGCCTGCCAGCGGGGTGCTACCACTAGCATGGG.....G.....T.....	873 8502
Query Sbjct	874 8503	AACACCATCACATGCTACGTGAAAGCCTAGCGGCTTGAAAGCTGCAGGGATAATCGC.....T.....C.....C..G.....G.T...	933 8562
Query Sbjct	934 8563	CCCACAATGCTGGTATGCGCGATGACTGGTGTACAGAAAGCCAGGGACCGAG.....C.....A.....T...	993 8622
Query Sbjct	994 8623	GAGGACGAGCGGAACCTGAGAGCCTCACGGAGGCTATGACCAGGTATTCTGCCCTCCT.....T.....	1053 8682
Query Sbjct	1054 8683	GGTGAccccccAGACCGGAGTATGATCT-GGAGCTGATAACATCTGCTCCTCAAATGT.....A.....T.....C..T.....	1112 8741
Query Sbjct	1113 8742	GTCTGTGGCGCTGGGCCACAAGGCCGCCAGATACTACCTGACCAGAGACCCCTACCAC.....T.....G.....	1172 8801
Query Sbjct	1173 8802	TCCAATGCCCGGGCTGCCCTGGAAACAGTTAGACACTCCCTGTCAATTCATGGCTGGG.....C.....	1232 8861
Query Sbjct	1233 8862	AAACATCATCCAGTACGCCCGACCATATGGGCTCGATGGCCTGTGACACACTTCTT.....A..G.G.....T..	1292 8921
Query Sbjct	1293 8922	CTCCATTCTCATGGCTCAAGACACGCTGGACCAGAACCTCAACTTGAGATGTACGGAGC.....C.....C.....T.....T.	1352 8981
Query Sbjct	1353 8982	GGTGTACTCCGTGAGTCCTTGGACCTCCAGCTATAATTGAAAGGTTACATGGCTTGA.....T.....C.....C.....C.....	1412 9041
Query Sbjct	1413 9042	CGCTTTTCTCTGCACACATACACTCCCCACGAACGTGACACGGGTGGCTTCAGCCCTCAG.....C..C.....G.....A.....	1472 9101
Query Sbjct	1473 9102	AAAACTTGGGCGCCACCCCTCAGAGCGTGGAAAGAGCCGGCACGTGCAGTCAGGGCGTC.....T.....G.....A.....	1532 9161
Query Sbjct	1533 9162	CCTCATCTCCGTGGGGGAGAGCGGCCGTGCGGTGATATCTCTTCAACTGGCGGT.....A.....G.....T.....G.....	1592 9221
Query Sbjct	1593 9222	GAAGACCAAGCTAAACTCACTCCATTGCCGGAGGCGCCTCTGGATTTATCCAGCTG.....A.....A.....T..	1652 9281
Query Sbjct	1653 9282	GTTCACCGTCGGCGCCGGGGGACATTATCACAGCGTGTGCGTGCCGACCACG.....T.....C..	1712 9341
Query Sbjct	1713 9342	C 1713 . 9342	

>gb|AF169003.1| Hepatitis C virus subtype 2a isolate G2aK1, complete genome  
Length=9693

Score = 2490 bits (1348), Expect = 0.0  
Identities = 1567/1680 (93%), Gaps = 6/1680 (0%)  
Strand=Plus/Plus

Query Sbjct	37 7697	ACTCCTTGTAGTCCCGAAGAGGAGAAGTTACCGATTAACCCCTTGAGCAACTCCCTGTTG.....C.....A.....G.....	96 7756
Query Sbjct	97 7757	CGATATCACAACAAGGTGTACTGTACCAACAAAGAGCGCCTCACTAAGGGCTAAAAG.....G..C.....T..T.....GC.....	156 7816
Query Sbjct	157 7817	GTAACTTTGATAGGATGCAAGTGCCTGACTCCTACTACGACTCAGTCTAAAGGACATT.....G.....T..T..T.....C	216 7876
Query Sbjct	217 7877	AAGCTAGCGGCCTCCAAGGTACCGCAAGGCTCCTCACCATGGAGGAGGCTGCCAGTTA.....G..G.....T.....A.....A..G	276 7936
Query Sbjct	277 7937	ACCCCACCCATTCTGCAAGATCTAAATATGGTTGGGCTAAGGAGGTCCGAGCTT.....T.....G.....A.....C.....	336 7996
Query Sbjct	337 7997	TCCGGGAGGGCCGTTAACACATCAAGTCCGTGGAAGGACCTCCTGGAGGACTCAGAA.....C.....A.....C..	396 8056
Query Sbjct	397 8057	ACACCAATTCCCACAACCATTATGCCAAAAATGAGGTGTTCTGCGTGGACCCACCAAG.....T..G..C.....C.....	456 8116
Query Sbjct	457 8117	GGGGGCAAGAAAGCAGCTCGCCTTATGTTACCTGACCTCGCGTCAGGGTCTGCGAG.....T.....C.....T.....	516 8176

Query Sbjct	517	AAGATGGCCCTTATGACATTACACAAAAACTCCTCAGGCGGTGATGGGGCTTCTTAT .....C.....TG.C.....G.....	576
Query Sbjct	577	GGATTCCAGTATTCCCCCGCTCAGCGGGTAGAGTTCTCTTGAAAGCATGGCGGAAAG ..C.....C.....A.....G.....C.....G.....	636
Query Sbjct	637	AAGGACCTATGGTTTTCGTATGATAACCGATGCTTGACTCAACCGTCACTGAGAGA ..A.....	696
Query Sbjct	697	GACATCAGGACTGAGGAGTCCATATATCGGGCCTGCTCCTGCCAGGGAGGCCACACT .....Y..A.....A.....C.....C..Y.....	756
Query Sbjct	757	GCCATACACTCGCTAACTGAGAGACTTACGTGGGAGGGCCTATGTTAACAGCAAGGGC .....T.....G.....G.....C.....	816
Query Sbjct	817	CAAACCTGCGGGTACAGCGTTGCCGCCAGCGGGTGCTCACCACTAGCATGGGAAC ..G.....	8536
Query Sbjct	877	ACCATCACATGCTACGTGAAAGCCTTAGCGGTTGTAAAGCTGCAGGGATAATCGCGCC .....R.....C.....C..G.....G.....G.T..A...	936
Query Sbjct	937	ACAATGCTGGTATGCGCGATGACTTGGTTGTCATCTCAGAAAGCCAGGGACCGAGGAG .....C.....C.....T.....	996
Query Sbjct	997	GACGAGCGAACCTGAGAGCCTTCACGGAGGCTATGACCAGGTATTCTGCCCT-CCTGG .....T.....Y.....	1055
Query Sbjct	1056	TGACcccccccAGACCGGAGTATGATCTGGAGCTGATAACATCTGCTCCTCAAATGTGTC C.....A.....C.....T.....	1115
Query Sbjct	1116	TGTGGCGCTGGG-CCCACAAGGCCCGCAGATACTACCTGACCAGAGACCCCTACCACTC .....A.-..A.....G.....	1174
Query Sbjct	1175	CAATCGCCCGGGCTGCCTGGAAACAGTTAGACACTCCCTGTCAATTGATGGCTGGGAA .....C.....T.....	1234
Query Sbjct	1235	ACATCATCCAGTACGCCCGACCATATGGGCTCGATGGCCTGATGACACACTTCTTCT .....T..A..T.....T..T.....	1294
Query Sbjct	1295	CCATTCTCATGGCTCAAGACACGCTGGACCAGAACCTCAACTTGAGATGTACGGAGCGG .....C.....C.....A.....T...	1354
Query Sbjct	1355	TGTACTCCGTGAGTCCCTT-GGACCTCCCAGCTATAATTGAAAGTTACATGGCTTGAC .....C.....C.....C.....	1413
Query Sbjct	1414	GCTTTTCTCTGCACACATACACTCCCCACGAACCTGACACGGGTGGCTTCAGCCCTCAGA ..C..C.....G.....	1473
Query Sbjct	1474	AAACTTGGGGGCCACCCCTCAGAGCGTGGAGAGGCCGGCACGTGCAGTCAGGGCGTCC .....T.....G.....	9193
Query Sbjct	1534	CTCATCTCCCGTGGGGGAGAGCGGCCGTGCGGTGATATCTCTTCAACTGGCGGTG .....A..A..G.....T.....C..G.....	1593
Query Sbjct	1594	AAGACCAAGCTAAACTCACTCCATTGCCGGAGGCACGTGCAAGTCCAGCTGG ..K.....A.....	9313
Query Sbjct	1654	TTCACCGTCGGCGCCGGGGGGCGACATTATCACAGCGTGTGCGTGCCGACACGC ..T.....T..T.....C...	1713
	9314		9373

>dbj|AB047640.1| Hepatitis C virus gene for polyprotein, complete cds, clone:JCH-1  
Length=9674

Score = 2488 bits (1347), Expect = 0.0  
Identities = 1591/1711 (92%), Gaps = 8/1711 (0%)  
Strand=Plus/Plus

Query Sbjct	7	ATGTCGTATACATGGACAGGCGCCT-TGATCACTCCTGTAGTCCGAAGAGGGAGAAGTT .....A..T.C.....C..-..G..C.A..A.....C.....A.....	65
Query Sbjct	66	ACCGATTAACCCCTTGAGCAACTCCCTGTTGCGATATCACAACAAGGTGTACTGTACCAAC G..A.....T.....G.....C..T.....A.....T..	125
Query Sbjct	126	AACAAAGAGCGCCTCACTAAGGCTAAAAGGTAACCTTGATAGGATGCAAGTGCCTGA ..T.....T.....	185
Query Sbjct	186	CTCCTACTACGACTCAGTCTAAAGGACATTAAGCTAGCGGCCTCCAAGGTACCGCAAG ..G.....T..T.....C.....G.....	245
	7849		7908

Query Sbjct	246 7909	GCTCCTCACCATGGAGGAGGCTTGCAGTTAACCCACCCATTCTGCAAGATCTAAATA .....T.A.....G....A..G.....C.....C..G..	305 7968
Query Sbjct	306 7969	TGGGTTTGGGGCTAAGGAGGTCCGCAGCTTGTCCGGAGGGCCGTTAACACATCAAGTC .....C.....	365 8028
Query Sbjct	366 8029	CGTGTGGAAGGACCTCCTGGAGGACTCAGAAACACCAATTCCCACAACCATTATGCCAA .....T....A.....C.....T.....C.....	425 8088
Query Sbjct	426 8089	AAATGAGGTGTTCTGCCTGGACCCCACCAAGGGGGCAAGAAAGCAGCTGCCTTATCGT .....G.....T..A...C.....	485 8148
Query Sbjct	486 8149	TTACCCCTGACCTCGCGTCAGGGCTCGAGAAGATGGCCTTATGACATTACACAAAA .....TG.C.....	545 8208
Query Sbjct	546 8209	ACTTCCTCAGGCCGTGATGGGGCTTCTTATGGATTCCAGTATTCCCCGCTCAGCGGGT G.....C.....C.....	605 8268
Query Sbjct	606 8269	AGAGTTCTCTTGAAGCATGGCGGAAAGA-AGGACCTATGGTTTTCGTATGATA G.....G.....G.....	664 8327
Query Sbjct	665 8328	CCCGATGCTTGACTCAACCGTCACTGAGAGAGACATCAGGACTGAGGAGTCCATATATC .....C.	724 8387
Query Sbjct	725 8388	GGGCCTGCTCCTGCCAGGGAGGCC-ACACTGCCATACACTCGCTAACTGAGAGACTT A.....A.....G.....G.....C.....	783 8446
Query Sbjct	784 8447	TACGTGGAGGGCTATGTTAACAGCAAGGCCAACCTGCAGGTACAGCGTTGCCGC ..T.....C.....GT.....	843 8506
Query Sbjct	844 8507	GCCAGCGGGTGCTCACCACTAGCATGGGAACACCATCACATGCTACGTGAAAGCCTTA .....T.....T.....T..A.....C..	903 8566
Query Sbjct	904 8567	GCGGCTTGTAAAGCTGCAGGGATAATCGGCCAACATGCTGGTATGCGGCATGACTTG .....C..G.....G.....T.....G.....C.....	963 8626
Query Sbjct	964 8627	GTTGTCATCTCAGAAAGCCAGGGACCGAGGAGACGAGCGAACCTGAGAGCCTTCACG ..C.....T.....	1023 8686
Query Sbjct	1024 8687	GAGGCTATGACCAGGTATTCTGCCCTCCTGGTGA.....AGACCGGAGTATGATCTG .....A.....C..	1083 8746
Query Sbjct	1084 8747	GAGCTGATAACATCTGCTCCTCAAATGTGTCGTGGCGCTGGGCCACAAGGCCGCC .....A.....T.....C.....A..T.....G.....	1143 8806
Query Sbjct	1144 8807	AGATACTACCTGACCAGAGACCCCTACCACTCCAATGCCCGGGCTGCCTGGAAACAGTT .....C.....T.....T.....	1203 8866
Query Sbjct	1204 8867	AGACACTCCCCGTCAATTGATGGCTGGAAACATCATCCAGTACGCCCGACCATATGG .....T.....T.....T..A.....	1263 8926
Query Sbjct	1264 8927	GCTCGCATGGCCTGATGACACACTTCTCTCCATTCTCATGGCTCAAGACACGCTGGAC ..T.....C..G.....C..A...	1323 8986
Query Sbjct	1324 8987	CAGAACCTCAACTTGAGATGTACGGAGCGGTGTACTCCGTGAGTCC-CTTGGACCTCCC .....T.....A.....T.....T.....	1382 9045
Query Sbjct	1383 9046	AGCTATAATTGAAAGGTTACATGGCTTGACGCTTTCTCTGCACACATACACTCCCCA ...C.....C.....C..C.....	1442 9105
Query Sbjct	1443 9106	CGAACTGACACGGGTGGCTCAGCCCTCAGAAAACCTGGGCGCCACCCCTCAGAGCGTG .....G.....	1502 9165
Query Sbjct	1503 9166	GAAGAGCCGGCACGTGCAGTCAGGGCGTCCCTCATCTCCGTGGGGGAGAGCGGCCGT .....T.....G.....T.....G.....	1562 9225
Query Sbjct	1563 9226	CTCGGGTCGATATCTCTCAACTGGCGGTGAAGACCAAGCTCAAACACTCCATTGCC T.....G..C.....T.....	1622 9285
Query Sbjct	1623 9286	GGAGGGCGCGCCTCTGGATTATCCAGCTGGTCACCGTCGGCGCCGGCGACAT .....A.....G.....T.....T.....	1682 9345
Query Sbjct	1683 9346	TTATCACAGCGTGTGCGTGCCTGGACACGC .....C... 1713 .....C... 9376	

>gb|AF238482.1| Hepatitis C virus subtype 2a strain MD2a-2, complete genome  
Length=9416

Score = 2477 bits (1341), Expect = 0.0  
Identities = 1570/1682 (93%), Gaps = 10/1682 (0%)

# BLAST Basic Local Alignment Search Tool

Job Title: Nucleotide sequence (1713 letters)

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BLASTX 2.2.17 (Aug-26-2007)

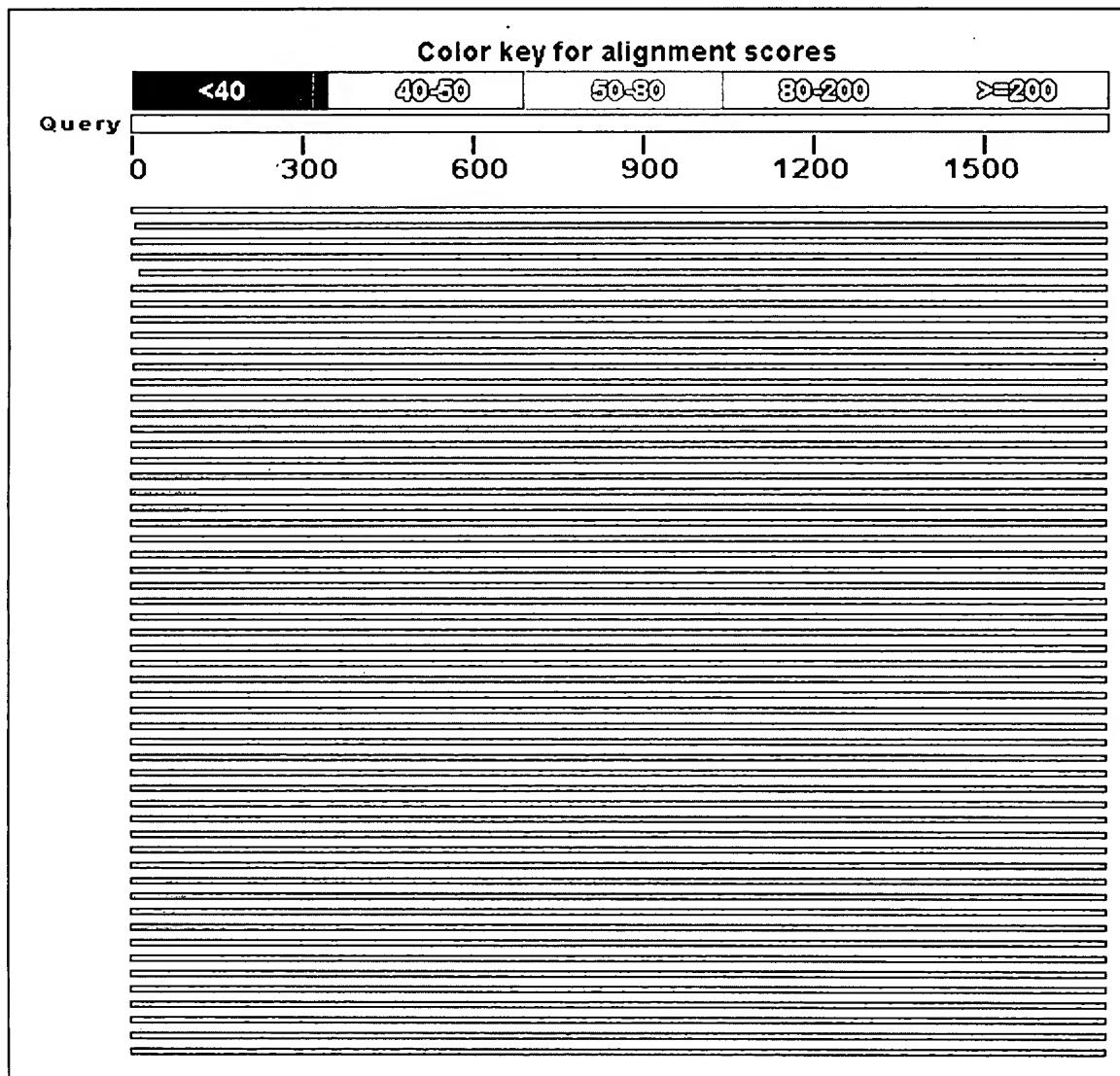
**Reference:** Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402. RID: HT70ANZ5013 **Database:** All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects 5,585,305 sequences; 1,931,637,290 total letters

Query= Length=1713

SEQ ID NO: 6 (v protein database)

## Distribution of 100 Blast Hits on the Query Sequence

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## Sequences producing significant alignments:

		Score (Bits)	E Value
ref YP_001469630.1	polyprotein [Hepatitis C virus genotype 2...	1122	0.0
gb AYA24375.1	polyprotein [Hepatitis C virus]	1119	0.0
gb AYA24373.1	polyprotein [Hepatitis C virus]	1119	0.0
sp P26660 POLG HCVJ6	Genome polyprotein [Contains: Core prote...	1113	0.0
gb AYA24374.1	polyprotein [Hepatitis C virus]	1110	0.0
dbj BAB32874.1	polyprotein [Hepatitis C virus]	1108	0.0
pdb 1YUY A	Chain A, Hepatitis C Virus Ns5b Rna-Dependent Rna ...	1107	0.0
gb AAF59943.1 AF238484_1	polyprotein [Hepatitis C virus subtype	1102	0.0
gb AAF25613.1 AF169005_1	polyprotein [Hepatitis C virus subtype	1100	0.0
gb AAF59942.1 AF238483_1	polyprotein [Hepatitis C virus subtype	1100	0.0
dbj BAB32877.1	polyprotein [Hepatitis C virus]	1100	0.0
gb AAF59940.1 AF238481_1	polyprotein [Hepatitis C virus subtype	1098	0.0
dbj BAB32873.1	polyprotein [Hepatitis C virus]	1095	0.0
gb AAU89634.1	polyprotein [Hepatitis C virus subtype 2a]	1090	0.0
gb AAF59944.1 AF238485_1	polyprotein [Hepatitis C virus subtype	1084	0.0
dbj BAB32878.1	polyprotein [Hepatitis C virus]	1083	0.0
gb AAF59941.1 AF238482_1	polyprotein [Hepatitis C virus subtype	1082	0.0
gb AAF25611.1 AF169003_1	polyprotein [Hepatitis C virus subtype	1080	0.0
dbj BAD06942.1	hepatitis C virus nonstructural protein [Hepatit	1080	0.0
sp Q99IB8 POLG HCVJF	Genome polyprotein [Contains: Core prote...	1080	0.0
dbj BAB32875.1	polyprotein [Hepatitis C virus]	1079	0.0
gb AAF25610.1 AF169002_1	polyprotein [Hepatitis C virus subtype	1078	0.0
dbj BAB32876.1	polyprotein [Hepatitis C virus]	1077	0.0
gb AAF25612.1 AF169004_1	polyprotein [Hepatitis C virus subtype	1069	0.0
gb AAZ85047.1	polyprotein [Hepatitis C virus (isolate D54)]	1028	0.0
sp Q68749 POLG HCVBB	Genome polyprotein [Contains: Core prote...	1023	0.0
sp Q9QAX1 POLG HCVVA	Genome polyprotein [Contains: Core prote...	1019	0.0
gb AAP55701.1	polyprotein [Hepatitis C virus subtype 2b]	1016	0.0
gb AAP55702.1	polyprotein [Hepatitis C virus subtype 2b]	1015	0.0
gb ABR18853.1	polyprotein [Hepatitis C virus]	1015	0.0
gb AAP55699.1	polyprotein [Hepatitis C virus subtype 2b]	1014	0.0
gb AAP55700.1	polyprotein [Hepatitis C virus subtype 2b]	1014	0.0
gb ABR18852.1	polyprotein [Hepatitis C virus]	1014	0.0
gb AAP55694.1	polyprotein [Hepatitis C virus subtype 2b]	1013	0.0
gb AAP55686.1	polyprotein [Hepatitis C virus subtype 2b]	1013	0.0
gb AAP55693.1	polyprotein [Hepatitis C virus subtype 2b]	1012	0.0
gb AAP55688.1	polyprotein [Hepatitis C virus subtype 2b]	1010	0.0
gb AAP55685.1	polyprotein [Hepatitis C virus subtype 2b]	1010	0.0
gb AAP55698.1	polyprotein [Hepatitis C virus subtype 2b]	1009	0.0
gb AAP55697.1	polyprotein [Hepatitis C virus subtype 2b]	1009	0.0
gb AAP55704.1	polyprotein [Hepatitis C virus subtype 2b]	1009	0.0
sp P26661 POLG HCVJ8	Genome polyprotein [Contains: Core prote...	1009	0.0
gb AAF59945.1 AF238486_1	polyprotein [Hepatitis C virus subtype	1007	0.0
gb AAP55691.1	polyprotein [Hepatitis C virus subtype 2b]	1006	0.0
gb AAP55696.1	polyprotein [Hepatitis C virus subtype 2b]	1006	0.0
gb AAP55695.1	polyprotein [Hepatitis C virus subtype 2b]	1005	0.0
gb AAP55703.1	polyprotein [Hepatitis C virus subtype 2b]	1003	0.0
sp Q9DHD6 POLG HCVJP	Genome polyprotein [Contains: Core prote...	1000	0.0
gb AAP55692.1	polyprotein [Hepatitis C virus subtype 2b]	999	0.0
gb AAP55690.1	polyprotein [Hepatitis C virus subtype 2b]	997	0.0
gb AAP55689.1	polyprotein [Hepatitis C virus subtype 2b]	996	0.0
gb AAP55687.1	polyprotein [Hepatitis C virus subtype 2b]	986	0.0
gb ABV46232.1	polyprotein [Hepatitis C virus subtype 1b]	892	0.0
dbj BAC66797.1	RNA-dependent RNA polymerase [Hepatitis C virus]	892	0.0
dbj BAB18807.1	polyprotein [Hepatitis C virus]	892	0.0
gb ABV46228.1	polyprotein [Hepatitis C virus subtype 1b]	892	0.0
gb ABV46160.1	polyprotein [Hepatitis C virus subtype 1a]	892	0.0
dbj BAC66799.1	RNA-dependent RNA polymerase [Hepatitis C virus]	892	0.0
gb ABV46215.1	polyprotein [Hepatitis C virus subtype 1b]	891	0.0
dbj BAC66794.1	RNA-dependent RNA polymerase [Hepatitis C virus]	891	0.0
gb AAF65950.1 AF207760_1	polyprotein [Hepatitis C virus subtype	891	0.0

S

gb ABV46234.1	polyprotein [Hepatitis C virus subtype 1b]	890	0.0
gb ABV46226.1	polyprotein [Hepatitis C virus subtype 1b]	890	0.0
gb ABV46060.1	polyprotein [Hepatitis C virus subtype 1b]	890	0.0
sp Q9WMX2 POLG_HCVCO	Genome polyprotein [Contains: Core prote...]	890	0.0
emb CAB46913.1	non-structural polyprotein [Hepatitis C virus...]	890	0.0
emb CAB46911.1	non-structural polyprotein [Hepatitis C virus...]	890	0.0
gb ABV46237.1	polyprotein [Hepatitis C virus subtype 1b]	890	0.0
gb ABV46113.1	polyprotein [Hepatitis C virus subtype 1b]	890	0.0
gb ABR18850.1	polyprotein [Hepatitis C virus]	890	0.0
dbj BAC66820.1	RNA-dependent RNA polymerase [Hepatitis C virus]	890	0.0
dbj BAD73986.1	polyprotein [Hepatitis C virus subtype 1b]	890	0.0
ref YP_001469633.1	polyprotein [Hepatitis C virus genotype 5...]	890	0.0
gb ABV46259.1	polyprotein [Hepatitis C virus subtype 1a]	890	0.0
gb AAL00900.1	polyprotein [Hepatitis C virus subtype 1b]	890	0.0
gb ABV46302.1	polyprotein [Hepatitis C virus subtype 1b]	889	0.0
gb ABV46238.1	polyprotein [Hepatitis C virus subtype 1b]	889	0.0
gb ABV46065.1	polyprotein [Hepatitis C virus subtype 1b]	889	0.0
gb AAD56196.1 AF165061_1	polyprotein [Hepatitis C virus subtype	889	0.0
dbj BAA03905.1	polyprotein precursor [Hepatitis C virus genotyp	889	0.0
dbj BAC66804.1	RNA-dependent RNA polymerase [Hepatitis C virus]	889	0.0
dbj BAA08120.1	HCV polyprotein [Hepatitis C virus]	889	0.0
dbj BAA06303.1	polyprotein [Hepatitis C virus]	889	0.0
gb ABV46151.1	polyprotein [Hepatitis C virus subtype 1b]	889	0.0
gb ABV46068.1	polyprotein [Hepatitis C virus subtype 1b]	889	0.0
dbj BAC66818.1	RNA-dependent RNA polymerase [Hepatitis C virus]	889	0.0
gb AAF65949.1 AF207759_1	polyprotein [Hepatitis C virus subtype	889	0.0
sp P26662 POLG_HCVJA	Genome polyprotein [Contains: Core prote...]	889	0.0
gb ABV46116.1	polyprotein [Hepatitis C virus subtype 1b]	888	0.0
gb ABR27412.1	polyprotein [Hepatitis C virus]	888	0.0
dbj BAC66822.1	RNA-dependent RNA polymerase [Hepatitis C virus]	888	0.0
sp Q913V3 POLG_HCVR6	Genome polyprotein [Contains: Core prote...]	888	0.0
gb ABV46301.1	polyprotein [Hepatitis C virus subtype 1b]	888	0.0
gb ABV46283.1	polyprotein [Hepatitis C virus subtype 1b]	888	0.0
gb AAT40682.1	polyprotein [Hepatitis C virus]	888	0.0
gb AAF65960.1 AF207770_1	polyprotein [Hepatitis C virus subtype	888	0.0
dbj BAA25076.1	polyprotein [Hepatitis C virus]	888	0.0
sp Q91936 POLG_HCVSA	Genome polyprotein [Contains: Core prote...]	888	0.0
gb ABV46242.1	polyprotein [Hepatitis C virus subtype 1b]	887	0.0
gb ABV46233.1	polyprotein [Hepatitis C virus subtype 1b]	887	0.0

## Alignments

>ref|YP\_001469630.1| polyprotein [Hepatitis C virus genotype 2]  
 gb|AAF01178.1|AF177036\_1 polyprotein [Hepatitis C virus subtype 2a]  
 Length=3033

Score = 1122 bits (2903), Expect = 0.0  
 Identities = 569/570 (99%), Positives = 570/570 (100%), Gaps = 0/570 (0%)  
 Frame = +1

Query 4 Sbjct 2443	SMSYTWTGALITPCSPEEKLPINPLSNSLLRYHNKVYCTTKSASLRAKKVTFDRMQVL ....S.....	183 2502
Query 184 Sbjct 2503	DSYYDSVLKDIKLAASKVTARLLTMEECQLTPPHSARSKYGFGEAKEVRSLSGRAVNHIK .....	363 2562
Query 364 Sbjct 2563	SVWKDLLEDSETPIPTTIMAKNEVFCVDPTKGKKAAARLIVYPDLGVRVCEKMALYDITQ .....	543 2622
Query 544 Sbjct 2623	KLPQAVMGASYGFQYSPAQRVEFLLKAWAEKKDPMGFSYDTRCFDSTVTERDIRTEESIY .....	723 2682
Query 724 Sbjct 2683	RACSLPEEAHTAIHSLTERLYVGGPMFNSKGQTCGYRRCRASGVLTSMGNTITCYVkal .....	903 2742
Query 904 Sbjct 2743	aackaaagiiapTMLVCGDDLVVISESGTEEDERNLRAFTEAMTRYSAPPGDPRPEYDL .....	1083 2802

Query Sbjct	1084 2803	ELITSCSSNVSVALGPQGRRYYLTRDPTTPIARAAWETVRHSPVNSWLGNIIQYAPTIW .....	1263 2862
Query Sbjct	1264 2863	ARMVLMTHFFSILMAQDTLDQNLNFEMYGAVYSVSPLDLPPIIERLHGLDAFSLHTYTPH .....	1443 2922
Query Sbjct	1444 2923	ELTRVASALRKLGAPPLRAWKSRAVRAVLISRGGRAAVCGRYLFNWAVTKKLKLTPLP .....	1623 2982
Query Sbjct	1624 2983	EARL LDLSWFTVGAGGGDIYHSVSRARPR 1713 .....	3012

>gb|AY24375.1| polyprotein [Hepatitis C virus]  
Length=589

Score = 1119 bits (2894), Expect = 0.0  
Identities = 567/568 (99%), Positives = 568/568 (100%), Gaps = 0/568 (0%)  
Frame = +1

Query Sbjct	10 1	SYWTGALITPCSPEEKLPINPLSNSLLRYHNKVYCTTKSASLRAKKVTFDRMQVLD S .....	189 60
Query Sbjct	190 61	YYDSVLKDIKLAASKVTARLLTMEACQLTPPHSARS SKYGF GAKEVRSLSGRAVNHI KSV .....	369 120
Query Sbjct	370 121	WKDLLEDSETPIPTTIMAKNEVFCVDPTKGKKAARLIVYPDLGVRVCEK M ALYDITQKL .....	549 180
Query Sbjct	550 181	PQAVMGASYGFQYSPAQRVEFLLKAWAEKKDPMGFSYDTRCFDSTVTERDIRTEESIYRA .....	729 240
Query Sbjct	730 241	CSLPEEAHTAIHSLTERLYVGGPMFNSKGQTCGYRRCRASGVLTSMGNTITCYVkalaa .....	909 300
Query Sbjct	910 301	ckaagiliaPTMLVCGDDLVVISESQGTEEDERNLRAFTEAMTRYSAPPGDPPRPEYDLEL .....	1089 360
Query Sbjct	1090 361	ITSCSSNVSVALGPQGRRYYLTRDPTTPIARAAWETVRHSPVNSWLGNIIQYAPTIWAR .....	1269 420
Query Sbjct	1270 421	MVLMTHFFSILMAQDTLDQNLNFEMYGAVYSVSPLDLPPIIERLHGLDAFSLHTYTPHEL .....	1449 480
Query Sbjct	1450 481	TRVASALRKLGAPPLRAWKSRAVRAVLISRGGRAAVCGRYLFNWAVTKKLKLTPLPEA .....	1629 540
Query Sbjct	1630 541	RLLDLSSWFTVGAGGGDIYHSVSRARPR 1713 .....	568

>gb|AY24373.1| polyprotein [Hepatitis C virus]  
Length=591

Score = 1119 bits (2894), Expect = 0.0  
Identities = 567/570 (99%), Positives = 569/570 (99%), Gaps = 0/570 (0%)  
Frame = +1

Query Sbjct	4 1	SMSYTWTGALITPCSPEEKLPINPLSNSLLRYHNKVYCTTKSASLRAKKVTFDRMQV L .....	183 60
Query Sbjct	184 61	DSYYDSVLKDIKLAASKVTARLLTMEACQLTPPHSARS SKYGF GAKEVRSLSGRAVNHI K .....	363 120
Query Sbjct	364 121	SVWKDLLEDSETPIPTTIMAKNEVFCVDPTKGKKAARLIVYPDLGVRVCEK M ALYDITQ .....	543 180
Query Sbjct	544 181	KLPQAVMGASYGFQYSPAQRVEFLLKAWAEKKDPMGFSYDTRCFDSTVTERDIRTEESIY .....	723 240
Query Sbjct	724 241	RACSLPEEAHTAIHSLTERLYVGGPMFNSKGQTCGYRRCRASGVLTSMGNTITCYVkal .....	903 300
Query Sbjct	904 301	aackaagiliaPTMLVCGDDLVVISESQGTEEDERNLRAFTEAMTRYSAPPGDPPRPEYDL .....	1083 360
Query Sbjct	1084 361	ELITSCSSNVSVALGPQGRRYYLTRDPTTPIARAAWETVRHSPVNSWLGNIIQYAPTIW .....	1263 420
Query Sbjct	1264 421	ARMVLMTHFFSILMAQDTLDQNLNFEMYGAVYSVSPLDLPPIIERLHGLDAFSLHTYTPH .....	1443 480

Query 1444 ELTRVASALRKLGAPPLRAWKSRARAVRASLISRGGRAAVCGRYLFNWAVKTKLKLTPLP 1623  
 Sbjct 481 ..... 540

Query 1624 EARL LDLSWFTVGAGGGDIYHSVSRARPR 1713  
 Sbjct 541 ..... 570

>sp|P26660|POLG\_HCVJ6 Genome polyprotein [Contains: Core protein p21 (Capsid protein C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirus) (NS3P) (p70); Non-structural protein 4A (NS4A) (p8); Non-structural protein 4B (NS4B) (p27); Non-structural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]

dbj|BAA00792.1| polyprotein [Hepatitis C virus]

Length=3033

Score = 1113 bits (2878), Expect = 0.0  
 Identities = 562/570 (98%), Positives = 569/570 (99%), Gaps = 0/570 (0%)  
 Frame = +1

Query 4 SMSYWTGALITPCSPEEKLPINPLSNSLLRYHNKVYCTTKSASLRKKVTFDRMQVL 183  
 Sbjct 2443 ....S.....S.....A. 2502

Query 184 DSYYDSVLKDIKLAASKVTARLLTMEACQLTPPHSARSKYGFRAKEVRSLSGRAVNHIK 363  
 Sbjct 2503 .AH.....L..... 2562

Query 364 SVWKDLLEDSETPIPTTIMAKNEVFCVDPTKGGKKAARLIVYPDLGVRVCEKMALYDITQ 543  
 Sbjct 2563 .....TQ..... 2622

Query 544 KLPQAVMGASYGFQYSPAQRVEFLLKAWAEKKDPMGFSYDTRCFDSTVTERDIRTEESIY 723  
 Sbjct 2623 ..... 2682

Query 724 RACSLPEEAHTAIHSLTERLYVGGPMFNSKGQTCGYRRCRASGVLTSMGNTITCYVkal 903  
 Sbjct 2683 ..... 2742

Query 904 aackaagiaPTMLVCGDDLVVISESQGTEEDERNLRAFTEAMTRYSAPPGDPRPEYDL 1083  
 Sbjct 2743 ..... 2802

Query 1084 ELITSCSSNVSVALGPQGRRYYLTRDPTTPIARAAWETVRHSPVNSWLGNIIQYAPTIW 1263  
 Sbjct 2803 ..... 2862

Query 1264 ARMVLMTHFFSILMAQDTLDQNLNFEMYGAVYSVSPLDLPAAIERLHGLDAFSLHTYTPH 1443  
 Sbjct 2863 ..... 2922

Query 1444 ELTRVASALRKLGAPPLRAWKSRARAVRASLISRGGRAAVCGRYLFNWAVKTKLKLTPLP 1623  
 Sbjct 2923 ..... 2982

Query 1624 EARL LDLSWFTVGAGGGDIYHSVSRARPR 1713  
 Sbjct 2983 ..... 3012

>gb|AYY24374.1| polyprotein [Hepatitis C virus]  
 Length=586

Score = 1110 bits (2870), Expect = 0.0  
 Identities = 563/565 (99%), Positives = 564/565 (99%), Gaps = 0/565 (0%)  
 Frame = +1

Query 19 WTGALITPCSPEEKLPINPLSNSLLRYHNKVYCTTKSASLRKKVTFDRMQVLDYYD 198  
 Sbjct 1 .....H..... 60

Query 199 SVLKDIKLAASKVTARLLTMEACQLTPPHSARSKYGFRAKEVRSLSGRAVNHIKSVWKD 378  
 Sbjct 61 ..... 120

Query 379 LLEDSETPIPTTIMAKNEVFCVDPTKGGKKAARLIVYPDLGVRVCEKMALYDITQKLPQA 558  
 Sbjct 121 .....G..... 180

Query 559 VMGASYGFQYSPAQRVEFLLKAWAEKKDPMGFSYDTRCFDSTVTERDIRTEESIYRACSL 738  
 Sbjct 181 ..... 240

Query 739 PEEAHTAIHSLTERLYVGGPMFNSKGQTCGYRRCRASGVLTSMGNTITCYVkal aacka 918  
 Sbjct 241 ..... 300

Query 919 agiliaPTMLVCGDDLVVISESQGTEEDERNLRAFTEAMTRYSAPPGDPRPEYDLELITS 1098  
 Sbjct 301 ..... 360

Query 1099 CSSNVSVALGPQGRRYYLTRDPTTPIARAAWETVRHSPVNSWLGNIIQYAPTIWARMVL 1278  
 Sbjct 361 ..... 420

Query Sbjct	1279 421	MTHFFSILMAQDTLDQNLNFEMYGAVYSVSPLDPAIIERLHGLDAFSLHTYTPHELTRV .....	1458 480
Query Sbjct	1459 481	ASALRKLGAPPLRAWKSRARAVRASLISRGGRAAVCGRYLFNWAVKTKLKLTPEARLL .....	1638 540
Query Sbjct	1639 541	DLSSWFTVGAGGGDIYHSVSRARPR 1713 ..... 565	

>dbj|BAB32874.1| polyprotein [Hepatitis C virus]  
Length=3033

Score = 1108 bits (2867), Expect = 0.0  
Identities = 557/570 (97%), Positives = 568/570 (99%), Gaps = 0/570 (0%)  
Frame = +1

Query Sbjct	4 2443	SMSYTWTGALITPCSPEEKLPINPLSNSLLRYHNKVYCTTKSASLRACKVTFDRMQVL ....S.....S.....	183 2502
Query Sbjct	184 2503	DSYYDSVLKDIKLAASKVTARLLTMEACQLTPPHSARSKYGFGAKEVRSLSGRAVNHIK .A.....K..L.....	363 2562
Query Sbjct	364 2563	SVWKDLLEDSETPIPTTIMAKNEVFCVDPTKGGKKAARLIVYPDLGVRVCEKMALYDITQ .....Q.....V..	543 2622
Query Sbjct	544 2623	KLPQAVMGASYGFQYSPAQRVEFLLKAWAEKKDPMGFSYDTRCFDSTVTERDIRTEESIY .....T.....	723 2682
Query Sbjct	724 2683	RACSLPEEAHTAIHSLTERLYVGGPMFNSKGQTCGYRRCRASGVLTSMGNTITCYVkal .....S.....A..	903 2742
Query Sbjct	904 2743	aackaagiaPTMLVCGDDLVVISESQGTEEDERNLRAFTEAMTRYSAPPGDPPEYDL .....V.....	1083 2802
Query Sbjct	1084 2803	ELITSCSSNVSVALGPQGRRYYLTRDPTTPIARAAWETVRHSPVNSWLGNIIQYAPTIW .....A.....	1263 2862
Query Sbjct	1264 2863	ARMVLMTHFFSILMAQDTLDQNLNFEMYGAVYSVSPLDPAIIERLHGLDAFSLHTYTPH .....S..	1443 2922
Query Sbjct	1444 2923	ELTRVASALRKLGAPPLRAWKSRARAVRASLISRGGRAAVCGRYLFNWAVKTKLKLTPLP .....	1623 2982
Query Sbjct	1624 2983	EARLLDLSSWFTVGAGGGDIYHSVSRARPR 1713 ..... 3012	

>pdb|1YUY|A **S** Chain A, Hepatitis C Virus Ns5b Rna-Dependent Rna Polymerase  
Genotype 2a

**pdb|1YV2|A** **S** Chain A, Hepatitis C Virus Ns5b Rna-Dependent Rna Polymerase  
Genotype 2a

**pdb|1YVX|A** **S** Chain A, Hepatitis C Virus Rna Polymerase Genotype 2a In Complex  
With Non- Nucleoside Analogue Inhibitor

**pdb|1YVZ|A** **S** Chain A, Hepatitis C Virus Rna Polymerase Genotype 2a In Complex  
With Non- Nucleoside Analogue Inhibitor  
Length=570

Score = 1107 bits (2862), Expect = 0.0  
Identities = 557/570 (97%), Positives = 568/570 (99%), Gaps = 0/570 (0%)  
Frame = +1

Query Sbjct	4 1	SMSYTWTGALITPCSPEEKLPINPLSNSLLRYHNKVYCTTKSASLRACKVTFDRMQVL ....S.....S.....	183 60
Query Sbjct	184 61	DSYYDSVLKDIKLAASKVTARLLTMEACQLTPPHSARSKYGFGAKEVRSLSGRAVNHIK .A.....S..L.....	363 120
Query Sbjct	364 121	SVWKDLLEDSETPIPTTIMAKNEVFCVDPTKGGKKAARLIVYPDLGVRVCEKMALYDITQ .....Q.....V..	543 180
Query Sbjct	544 181	KLPQAVMGASYGFQYSPAQRVEFLLKAWAEKKDPMGFSYDTRCFDSTVTERDIRTEESIY .....	723 240
Query Sbjct	724 241	RACSLPEEAHTAIHSLTERLYVGGPMFNSKGQTCGYRRCRASGVLTSMGNTITCYVkal Q.....R.....S.....	903 300

Query Sbjct	904 301	aackaagiaPTMLVCGDDLVVISESQGTEEDERNLRAFTEAMTRY SAPP GDP PRPEYDL .....V.....	1083 360
Query Sbjct	1084 361	ELITSCSSNVSVALGPQGRRYYLTRDPTTPIARAAWETVRHSPVNSW LGNIIQYAPTIW .....	1263 420
Query Sbjct	1264 421	ARMVLMTHFFSILMAQDTLDQNLNFEMYGAVYVSPLDPAIIERLHGLDAFSLHTYTPH V.....S.....	1443 480
Query Sbjct	1444 481	ELTRVASALRKLGAPPLRAWKSRAVRA SLSRGGRAAVCGRYLFNWA VTKLKLTPLP .....	1623 540
Query Sbjct	1624 541	EARL LDLSWFTVGAGGGDIYHSVSRARPR 1713 ..... 570	

>gb|AAF59943.1|AF238484\_1 polyprotein [Hepatitis C virus subtype 2a]  
Length=3033

Score = 1102 bits (2849), Expect = 0.0  
Identities = 553/570 (97%), Positives = 567/570 (99%), Gaps = 0/570 (0%)  
Frame = +1

Query Sbjct	4 2443	SMSYWTGALITPCSPEEKLPINPLSNSLLRYHNKVYCTT KSASLRAK VTFDRMQVL ....S.....S.....T...	183 2502
Query Sbjct	184 2503	DSYYDSVLKDIKLAASKVTARLLT MEEACQLTPPHSAR SKYGF GAKEVRSLSGRAVNHIK .AH.....N....V.....	363 2562
Query Sbjct	364 2563	SVW KDLLEDSETPIPTT IMAKNEVFCVDPTKGGKKAARLIVY PDLGVRVCEK M ALYDITQ .....Q.....V..	543 2622
Query Sbjct	544 2623	KLPQAVMGASYGFQYSPAQRVEFLLKAWAEK KDPMGFSYDTRCFDSTVTERDIRTEESIY .....D.....R.....	723 2682
Query Sbjct	724 2683	RACSLPEEAHTAIHSLTERLYVGGPMFNSKGQTCGYRRCRASGV LTTSMGNTITCYVka1 Q.....R.....	903 2742
Query Sbjct	904 2743	aackaagiaPTMLVCGDDLVVISESQGTEEDERNLRAFTEAMTRY SAPP GDP PRPEYDL .....V.....I.....	1083 2802
Query Sbjct	1084 2803	ELITSCSSNVSVALGPQGRRYYLTRDPTTPIARAAWETVRHSPVNSW LGNIIQYAPTIW .....V.	1263 2862
Query Sbjct	1264 2863	ARMVLMTHFFSILMAQDTLDQNLNFEMYGAVYVSPLDPAIIERLHGLDAFSLHTYTPH .....S.....	1443 2922
Query Sbjct	1444 2923	ELTRVASALRKLGAPPLRAWKSRAVRA SLSRGGRAAVCGRYLFNWA VTKLKLTPLP .....	1623 2982
Query Sbjct	1624 2983	EARL LDLSWFTVGAGGGDIYHSVSRARPR 1713 ..... 3012	

>gb|AAF25613.1|AF169005\_1 polyprotein [Hepatitis C virus subtype 2a]  
Length=3033

Score = 1100 bits (2844), Expect = 0.0  
Identities = 551/570 (96%), Positives = 565/570 (99%), Gaps = 0/570 (0%)  
Frame = +1

Query Sbjct	4 2443	SMSYWTGALITPCSPEEKLPINPLSNSLLRYHNKVYCTT KSASLRAK VTFDRMQVL ....S.....S.....	183 2502
Query Sbjct	184 2503	DSYYDSVLKDIKLAASKVTARLLT MEEACQLTPPHSAR SKYGF GAKEVRSLSGRAVNHIK .AH.....S.....L.....	363 2562
Query Sbjct	364 2563	SVW KDLLEDSETPIPTT IMAKNEVFCVDPTKGGKKAARLIVY PDLGVRVCEK M ALYDITQ .....Q.....A.....V..	543 2622
Query Sbjct	544 2623	KLPQAVMGASYGFQYSPAQRVEFLLKAWAEK KDPMGFSYDTRCFDSTVTERDIRTEESIY .....	723 2682
Query Sbjct	724 2683	RACSLPEEAHTAIHSLTERLYVGGPMFNSKGQTCGYRRCRASGV LTTSMGNTITCYVka1 .....L.....I..	903 2742
Query Sbjct	904 2743	aackaagiaPTMLVCGDDLVVISESQGTEEDERNLRAFTEAMTRY SAPP GDP PRPEYDL .....V.....	1083 2802
Query Sbjct	1084 2803	ELITSCSSNVSVALGPQGRRYYLTRDPTTPIARAAWETVRHSPVNSW LGNIIQYAPTIW .....X.....LS.....	1263 2862

Query Sbjct	1264 2863	ARMVLMTHFFSILMAQDTLDQNLNFEMYGAVYSVSPLDLPかいERLHGLDAFSLHTYTPH V.....X.....S..	1443 2922
Query Sbjct	1444 2923	ELTRVASALRKLGAPPLRAWKSARAVRASLISRGGRAAVCGRYLFNWAVKTKLKLTPLP .....I.....	1623 2982
Query Sbjct	1624 2983	EARLLDLSSWFTVGAGGGDIYHSVSRARPR 1713 ..... 3012	

>gb|AAF59942.1|AF238483\_1 polyprotein [Hepatitis C virus subtype 2a]  
Length=3033

Score = 1100 bits (2844), Expect = 0.0  
Identities = 554/570 (97%), Positives = 566/570 (99%), Gaps = 0/570 (0%)  
Frame = +1

Query Sbjct	4 2443	SMSYTWTGALITPCSPEEKLPINPLSNSLLRYHNKVYCTTKSASLRAKKVTFDRMQVL .....S.....S.....	183 2502
Query Sbjct	184 2503	DSYYDSVLKDIKLAASKVTARLLTMEACQLTPPHSARSKYGFGAKEVRSLSGRAVNHIK .AH.....S.....L.....	363 2562
Query Sbjct	364 2563	SVWKDLLEDSETPIPTTIMAKNEVFCVDPTKGGKKAARLIVYPDLGVRVCEKMALYDITQ .....Q.....	543 2622
Query Sbjct	544 2623	KLPQAVMGASYGFQYSPAQRVEFLLKAWAEKKDPMGFSYDTRCFDSTVTERDIRTEESIY .....L.....	723 2682
Query Sbjct	724 2683	RACSLPEEAHTAIHSLTERLYVGGPMFNSKGQTCGYRRCRASGVLTSMGNTITCYVkal .....L.....S.....	903 2742
Query Sbjct	904 2743	aackaagiaPTMLVCGDDLVVISESQGTEEDERNLRAFTEAMTRYSAPPGDPRPEYDL .....V.....	1083 2802
Query Sbjct	1084 2803	ELITSCSSNVSVALGPQGRRYYLTRDPTTPIARAAWETVRHSPVNSWLGNIIQYAPTIW .....N.L.....	1263 2862
Query Sbjct	1264 2863	ARMVLMTHFFSILMAQDTLDQNLNFEMYGAVYSVSPLDLPかいERLHGLDAFSLHTYTPH .....S..	1443 2922
Query Sbjct	1444 2923	ELTRVASALRKLGAPPLRAWKSARAVRASLISRGGRAAVCGRYLFNWAVKTKLKLTPLP .....T.....	1623 2982
Query Sbjct	1624 2983	EARLLDLSSWFTVGAGGGDIYHSVSRARPR 1713 ..... 3012	

>dbj|BAB32877.1| polyprotein [Hepatitis C virus]  
Length=3033

Score = 1100 bits (2844), Expect = 0.0  
Identities = 551/569 (96%), Positives = 566/569 (99%), Gaps = 0/569 (0%)  
Frame = +1

Query Sbjct	7 2444	MSYTWTGALITPCSPEEKLPINPLSNSLLRYHNKVYCTTKSASLRAKKVTFDRMQVL ...S.....S.....	186 2503
Query Sbjct	187 2504	SYYDSVLKDIKLAASKVTARLLTMEACQLTPPHSARSKYGFGAKEVRSLSGRAVNHIKS A.....S.....L.....	366 2563
Query Sbjct	367 2564	VWKDLLEDSETPIPTTIMAKNEVFCVDPTKGGKKAARLIVYPDLGVRVCEKMALYDITQK .....Q.....V...	546 2623
Query Sbjct	547 2624	LPQAVMGASYGFQYSPAQRVEFLLKAWAEKKDPMGFSYDTRCFDSTVTERDIRTEESIYR .....D.RE.....Q	726 2683
Query Sbjct	727 2684	ACSLPEEAHTAIHSLTERLYVGGPMFNSKGQTCGYRRCRASGVLTSMGNTITCYVkala .....L.....A.....	906 2743
Query Sbjct	907 2744	aackaagiaPTMLVCGDDLVVISESQGTEEDERNLRAFTEAMTRYSAPPGDPRPEYDLE .....V.....	1086 2803
Query Sbjct	1087 2804	LITSCSSNVSVALGPQGRRYYLTRDPTTPIARAAWETVRHSPVNSWLGNIIQYAPTIWA .....V	1266 2863
Query Sbjct	1267 2864	RMVLMTHFFSILMAQDTLDQNLNFEMYGAVYSVSPLDLPかいERLHGLDAFSLHTYTPHE .....S.....S...	1446 2923
Query Sbjct	1447	LTRVASALRKLGAPPLRAWKSARAVRASLISRGGRAAVCGRYLFNWAVKTKLKLTPLP .....	1626

Sbjct	2924	.....	I.....	2983
Query	1627	ARLLDLSSWFTVGAGGGDIYHSVSRARPR	1713	
Sbjct	2984	.....	3012	

>gb|AAF59940.1|AF238481\_1 polyprotein [Hepatitis C virus subtype 2a]  
Length=3033

Score = 1098 bits (2840), Expect = 0.0  
Identities = 553/570 (97%), Positives = 563/570 (98%), Gaps = 0/570 (0%)  
Frame = +1

Query	4	SMSYWTGALITPCSPEEKLPINPLSNSLLRYHNKVYCTTKSASLRAKKVTFDRMQVL	183
Sbjct	2443	....S.....A.....	2502
Query	184	DSYYDSVLKDIKLAASKVTARLLTMEACQLTPPHSARSKYGFRAKEVRSLSGRAVNHIK	363
Sbjct	2503	.A.H.....S.....L.....	2562
Query	364	SVWKLLEDSETPIPTTIMAKNEVFCVDPTKGGKKAARLIVYPDLGVRVCEKMALYDITQ	543
Sbjct	2563	.....Q.....V..	2622
Query	544	KLPQAVMGASYGFQYSPAQRVEFLLKAWAEKKDPMGFSYDTRCFDSTVTERDIRTEESIY	723
Sbjct	2623	.....	2682
Query	724	RACSLPEEAHTAIHSLTERLYVGGPMFNSKGQTCGYRRCRASGVLTSMGNTITCYVkal	903
Sbjct	2683	L.....R.....	2742
Query	904	aackaagiaPTMLVCGDDLVVISESQGTEEDERNLRAFTEAMTRYSAPPGDPRPEYDL	1083
Sbjct	2743	.....V.....	2802
Query	1084	ELITSCSSNVSVALGPQGRRYYLTRDPTTPIARAAWETVRHSPVNSWLGNIIQYAPTIW	1263
Sbjct	2803	.....	2862
Query	1264	ARMVLMTHFFSILMAQDTLDQNLNFEMYGAVYSVSPLDPAIIERLHGLDAFSLHTYTPH	1443
Sbjct	2863	V.....S.....	2922
Query	1444	ELTRVASALRKLGAPPLRAWKSRARAVRASLISRGGRAAVCGRYLFNWAVTKLKLTPLP	1623
Sbjct	2923	.....T.....H.....I.....	2982
Query	1624	EARLLDLSSWFTVGAGGGDIYHSVSRARPR	1713
Sbjct	2983	.....	3012

>dbj|BAB32873.1| polyprotein [Hepatitis C virus]  
Length=3033

Score = 1095 bits (2833), Expect = 0.0  
Identities = 553/570 (97%), Positives = 564/570 (98%), Gaps = 0/570 (0%)  
Frame = +1

Query	4	SMSYWTGALITPCSPEEKLPINPLSNSLLRYHNKVYCTTKSASLRAKKVTFDRMQVL	183
Sbjct	2443	....S.....S.....S.....	2502
Query	184	DSYYDSVLKDIKLAASKVTARLLTMEACQLTPPHSARSKYGFRAKEVRSLSGRAVNHIK	363
Sbjct	2503	.A.....S.....L.....	2562
Query	364	SVWKLLEDSETPIPTTIMAKNEVFCVDPTKGGKKAARLIVYPDLGVRVCEKMALYDITQ	543
Sbjct	2563	.....Q.....A.....P.....V..	2622
Query	544	KLPQAVMGASYGFQYSPAQRVEFLLKAWAEKKDPMGFSYDTRCFDSTVTERDIRTEESIY	723
Sbjct	2623	.....R.....	2682
Query	724	RACSLPEEAHTAIHSLTERLYVGGPMFNSKGQTCGYRRCRASGVLTSMGNTITCYVkal	903
Sbjct	2683	Q.....R.....S.....	2742
Query	904	aackaagiaPTMLVCGDDLVVISESQGTEEDERNLRAFTEAMTRYSAPPGDPRPEYDL	1083
Sbjct	2743	.....	2802
Query	1084	ELITSCSSNVSVALGPQGRRYYLTRDPTTPIARAAWETVRHSPVNSWLGNIIQYAPTIW	1263
Sbjct	2803	.....S.....	2862
Query	1264	ARMVLMTHFFSILMAQDTLDQNLNFEMYGAVYSVSPLDPAIIERLHGLDAFSLHTYTPH	1443
Sbjct	2863	V.....S.....	2922
Query	1444	ELTRVASALRKLGAPPLRAWKSRARAVRASLISRGGRAAVCGRYLFNWAVTKLKLTPLP	1623
Sbjct	2923	.....	2982
Query	1624	EARLLDLSSWFTVGAGGGDIYHSVSRARPR	1713
Sbjct	2983	.....	3012